

**STIC Biotechnology Systems Branch**

**RAW SEQUENCE LISTING**  
**ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

10/522,106

Source:

PCT

Date Processed by STIC:

2-2-05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05



PCT

## RAW SEQUENCE LISTING

DATE: 02/02/2005

PATENT APPLICATION: US/10/522,106

TIME: 15:31:41

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\02022005\J522106.raw

2 <110> APPLICANT: Kogel, Karl-Heinz  
 3 Huckelhoven, Ralph  
 4 Trujillo, Marco  
 6 <120> TITLE OF INVENTION: Method for Obtaining a Pathogen Resistance in Plants  
 8 <130> FILE REFERENCE: 532622010500  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/522,106  
 11 <141> CURRENT FILING DATE: 2005-01-24  
 13 <160> NUMBER OF SEQ ID NOS: 24  
 14 <170> SOFTWARE: PatentIn Ver. 2.1

## ERRORED SEQUENCES

45 <210> SEQ ID NO: 2  
 46 <211> LENGTH: 112  
 47 <212> TYPE: PRT  
 48 <213> ORGANISM: Hordeum vulgare  
 W--> 49 <400> SEQUENCE: 2  
 50 Phe Lys Gly Ile Met Asn Glu Ile Ala Glu Leu Asp Gln Arg Asn Ile on  
 51 1 5 10 15  
 52 Ile Glu Met His Asn Tyr Leu Thr Ser Val Tyr Glu Glu Gly Asp Ala  
 53 20 25 30  
 54 Arg Ser Ala Leu Ile Thr Met Leu Gln Ala Leu Asn His Ala Lys Asn  
 55 35 40 45  
 E--> 56 Gly Val Asp Val Val Ser Xaa Thr Arg Val Arg Thr His Phe Ala Arg  
 57 50 55 60  
 58 Pro Asn Phe Lys Arg Val Leu Ser Lys Val Ala Ala Lys His Pro Tyr  
 59 65 70 75 80  
 60 Ala Lys Ile Gly Val Phe Tyr Cys Gly Ala Pro Val Leu Ala Gln Glu  
 61 85 90 95  
 62 Leu Ser Asn Leu Cys His Glu Phe Asn Gly Lys Cys Thr Thr Lys Phe  
 63 100 105 110  
 2181 <210> SEQ ID NO: 16  
 2182 <211> LENGTH: 939  
 2183 <212> TYPE: PRT  
 2184 <213> ORGANISM: Nicotiana tabacum  
 W--> 2185 <400> SEQUENCE: 16  
 2186 Met Gln Asn Ser Glu Asn His His Pro His His Gln His His His Ser  
 2187 1 5 10 15  
 2188 Asp Thr Glu Ile Ile Gly Asn Asp Arg Ala Ser Tyr Ser Gly Pro Leu  
 2189 20 25 30  
 2190 Ser Gly Pro Leu Asn Lys Arg Gly Gly Lys Lys Ser Ala Arg Phe Asn  
 2191 35 40 45

pls explain  
 "Xaa" location. Does Not Comply  
 Corrected Diskette Needed  
 (P5.1, 3)  
 See error explanation  
 on page 5.

## RAW SEQUENCE LISTING

DATE: 02/02/2005

PATENT APPLICATION: US/10/522,106

TIME: 15:31:42

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\02022005\J522106.raw

```

2192 Ile Pro Glu Ser Thr Asp Ile Gly Thr Ser Val Gly Thr Gly Gly Lys
2193      50                      55                      60
2194 Ser Asn Asp Asp Ala Tyr Val Glu Ile Thr Leu Asp Val Arg Glu Asp
2195 65                      70                      75                      80
2196 Ser Val Ala Val His Ser Val Lys Thr Ala Gly Gly Asp Asp Val Glu
2197                      85                      90                      95
2198 Asp Pro Glu Leu Ala Leu Leu Ala Lys Gly Leu Glu Lys Lys Ser Thr
2199                      100                     105                     110
2200 Leu Gly Ser Ser Leu Val Arg Asn Ala Ser Ser Arg Ile Arg Gln Val
2201                      115                     120                     125
2202 Ser Gln Glu Leu Arg Arg Leu Ala Ser Leu Asn Lys Arg Pro Ile Pro
2203                      130                     135                     140
2204 Thr Gly Arg Phe Asp Arg Asn Lys Ser Ala Ala Ala His Ala Leu Lys
2205 145                      150                      155                      160
2206 Gly Leu Lys Phe Ile Ser Lys Thr Asp Gly Gly Ala Gly Trp Ala Ala
2207                      165                      170                      175
2208 Val Glu Lys Arg Phe Asp Glu Ile Thr Ala Ser Thr Thr Gly Leu Leu
2209                      180                      185                      190
2210 Pro Arg Ala Lys Phe Gly Glu Cys Ile Gly Met Asn Lys Glu Ser Lys
2211                      195                     200                     205
2212 Glu Phe Ala Val Glu Leu Tyr Asp Ala Leu Ala Arg Arg Arg Asn Ile
2213                      210                     215                     220
2214 Thr Thr Asp Ser Ile Asn Lys Ala Gln Leu Lys Glu Phe Trp Asp Gln
2215 225                      230                      235                      240
2216 Val Ala Asp Gln Ser Phe Asp Ser Arg Leu Gln Thr Phe Phe Asp Met
2217                      245                      250                      255
2218 Val Asp Lys Asp Ala Asp Gly Arg Ile Thr Glu Glu Glu Val Arg Glu
2219                      260                      265                      270
2220 Ile Ile Gly Leu Ser Ala Ser Ala Asn Arg Leu Ser Thr Ile Gln Lys
2221                      275                      280                      285
2222 Gln Ala Asp Glu Tyr Ala Ala Met Ile Met Glu Glu Leu Asp Pro Asn
2223                      290                      295                      300
2224 Asn Leu Gly Tyr Ile Met Ile Glu Asn Leu Glu Met Leu Leu Leu Gln
2225 305                      310                      315                      320
2226 Ala Pro Asn Gln Ser Val Gln Arg Gly Gly Glu Ser Arg Asn Leu Ser
2227                      325                      330                      335
2228 Gln Met Leu Ser Gln Lys Leu Lys His Thr Gln Glu Arg Asn Pro Ile
2229                      340                      345                      350
2230 Val Arg Trp Tyr Lys Ser Phe Met Tyr Phe Leu Leu Asp Asn Trp Gln
2231                      355                      360                      365
2232 Arg Val Trp Val Leu Leu Leu Trp Ile Gly Ile Met Ala Gly Leu Phe
2233                      370                      375                      380
2234 Thr Trp Lys Tyr Ile Gln Tyr Lys Glu Lys Ala Ala Tyr Lys Val Met
2235 385                      390                      395                      400
2236 Gly Pro Cys Val Cys Phe Ala Lys Gly Ala Ala Glu Thr Leu Lys Leu
2237                      405                      410                      415
2238 Asn Met Ala Ile Ile Leu Phe Pro Val Cys Arg Asn Thr Ile Thr Trp
2239                      420                      425                      430
2240 Leu Arg Asn Lys Thr Arg Leu Gly Ala Ala Val Pro Phe Asp Asp Asn

```

## RAW SEQUENCE LISTING

DATE: 02/02/2005

PATENT APPLICATION: US/10/522,106

TIME: 15:31:42

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\02022005\J522106.raw

2241 435 440 445  
 2242 Leu Asn Phe His Lys Val Ile Ala Val Ala Ile Ala Leu Gly Val Gly  
 2243 450 455 460  
 2244 Ile His Gly Leu Ser His Leu Thr Cys Asp Phe Pro Arg Leu Leu Asn  
 2245 465 470 475 480  
 2246 Ala Ser Glu Glu Glu Tyr Glu Pro Met Lys Tyr Tyr Phe Gly Asp Gln  
 2247 485 490 495  
 2248 Pro Glu Ser Tyr Trp Trp Phe Ile Lys Gly Val Glu Gly Val Thr Gly  
 2249 500 505 510  
 2250 Ile Ile Met Val Val Leu Met Ala Ile Ala Phe Thr Leu Ala Thr Pro  
 2251 515 520 525  
 2252 Trp Phe Arg Arg Asn Arg Val Ser Leu Pro Lys Pro Phe His Lys Leu  
 2253 530 535 540  
 E--> 2254 Thr Gly Xaa Asn Ala Phe Trp Tyr Ser His His Leu Phe Val Ile Val  
 2255 545 550 555 560  
 2256 Tyr Thr Leu Phe Ile Val His Gly Glu Lys Leu Tyr Ile Thr Lys Asp  
 2257 565 570 575  
 2258 Trp Tyr Lys Arg Thr Asp Met Asp Val Leu Leu Thr Ile Pro Ile Ile  
 2259 580 585 590  
 2260 Leu Tyr Ala Ser Glu Arg Leu Ile Arg Ala Phe Arg Ser Ser Ile Lys  
 2261 595 600 605  
 2262 Ala Val Lys Ile Leu Lys Val Ala Val Tyr Pro Gly Asn Val Leu Ala  
 2263 610 615 620  
 2264 Leu His Met Ser Lys Pro Gln Gly Tyr Lys Tyr Lys Ser Gly Gln Tyr  
 2265 625 630 635 640  
 2266 Met Phe Val Asn Cys Ala Ala Val Ser Pro Phe Glu Trp His Pro Phe  
 2267 645 650 655  
 2268 Ser Ile Thr Ser Ala Pro Gly Asp Asp Tyr Leu Ser Val His Ile Arg  
 2269 660 665 670  
 2270 Thr Leu Gly Asp Trp Thr Arg Gln Leu Lys Thr Val Phe Ser Glu Val  
 2271 675 680 685  
 2272 Cys Gln Pro Pro Pro Asn Gly Lys Ser Gly Leu Leu Arg Ala Asp Tyr  
 2273 690 695 700  
 2274 Leu Gln Gly Glu Asn Asn Pro Asn Phe Pro Arg Val Leu Ile Asp Gly  
 2275 705 710 715 720  
 2276 Pro Tyr Gly Ala Pro Ala Gln Asp Tyr Lys Lys Tyr Glu Val Val Leu  
 2277 725 730 735  
 2278 Leu Val Gly Leu Gly Ile Gly Ala Thr Pro Met Ile Ser Ile Val Lys  
 2279 740 745 750  
 2280 Asp Ile Val Asn Asn Met Lys Ala Met Asp Glu Glu Glu Asn Ser Leu  
 2281 755 760 765  
 2282 Glu Asp Gly His Asn Asn Asn Met Ala Pro Asn Ser Ser Pro Asn Ile  
 2283 770 775 780  
 2284 Ala Lys Asn Lys Gly Asn Lys Ser Gly Ser Ala Ser Gly Gly Asn Asn  
 2285 785 790 795 800  
 2286 Phe Asn Thr Arg Arg Ala Tyr Phe Tyr Trp Val Thr Arg Glu Gln Gly  
 2287 805 810 815  
 2288 Ser Phe Asp Trp Phe Lys Gly Ile Met Asn Glu Ala Ala Glu Met Asp  
 2289 820 825 830

←  
 pls  
 explain  
 Xaa location.

pls see  
 error  
 explanation  
 on page 5.

The type of errors shown exist throughout  
 the Sequence Listing. Please check subsequent  
 sequences for similar errors.

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/522,106

DATE: 02/02/2005

TIME: 15:31:42

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\02022005\J522106.raw

2290 His Lys Gly Val Ile Glu Met His Asn Tyr Cys Thr Ser Val Tyr Glu  
2291 835 840 845  
2292 Glu Gly Asp Ala Arg Ser Ala Leu Ile Thr Met Leu Gln Ser Leu His  
2293 850 855 860  
2294 His Ala Lys Asn Gly Val Asp Ile Val Ser Gly Thr Arg Val Lys Ser  
2295 865 870 875 880  
2296 His Phe Ala Lys Pro Asn Trp Arg Asn Val Tyr Lys Arg Ile Ala Leu  
2297 885 890 895  
2298 Asn His Pro Glu Ala Lys Val Gly Val Phe Tyr Cys Gly Ala Pro Ala  
2299 900 905 910  
2300 Leu Thr Lys Glu Leu Arg Gln His Ala Leu Asp Phe Ser His Lys Thr  
2301 915 920 925  
2302 Ser Thr Lys Phe Asp Phe His Lys Glu Asn Phe  
2303 930 935

## VARIABLE LOCATION SUMMARY

DATE: 02/02/2005

PATENT APPLICATION: US/10/522,106

TIME: 15:31:43

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\02022005\J522106.raw,

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:1; Xaa Pos. 55

Seq#:2; Xaa Pos. 55

Seq#:15; N Pos. 1952

Seq#:15; Xaa Pos. 547

Seq#:16; Xaa Pos. 547

## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/522,106

DATE: 02/02/2005

TIME: 15:31:43

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\02022005\J522106.raw

L:10 M:270 C: Current Application Number differs; Replaced Current Application Number  
L:15 M:283 W: Missing Blank Line separator, <210> field identifier  
L:19 M:283 W: Missing Blank Line separator, <220> field identifier  
L:23 M:283 W: Missing Blank Line separator, <400> field identifier  
L:34 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:193  
L:49 M:283 W: Missing Blank Line separator, <400> field identifier  
L:56 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2  
L:69 M:283 W: Missing Blank Line separator, <220> field identifier  
L:73 M:283 W: Missing Blank Line separator, <400> field identifier  
L:255 M:283 W: Missing Blank Line separator, <400> field identifier  
L:379 M:283 W: Missing Blank Line separator, <220> field identifier  
L:383 M:283 W: Missing Blank Line separator, <400> field identifier  
L:570 M:283 W: Missing Blank Line separator, <400> field identifier  
L:698 M:283 W: Missing Blank Line separator, <220> field identifier  
L:702 M:283 W: Missing Blank Line separator, <400> field identifier  
L:904 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1032 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1036 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1234 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1364 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1368 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1556 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1680 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1684 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1868 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1990 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1994 M:283 W: Missing Blank Line separator, <400> field identifier  
L:2102 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:1935  
M:341 Repeated in SeqNo=15  
L:2185 M:283 W: Missing Blank Line separator, <400> field identifier  
L:2254 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:16  
L:2309 M:283 W: Missing Blank Line separator, <220> field identifier  
L:2313 M:283 W: Missing Blank Line separator, <400> field identifier  
L:2477 M:283 W: Missing Blank Line separator, <400> field identifier  
L:2589 M:283 W: Missing Blank Line separator, <220> field identifier  
L:2593 M:283 W: Missing Blank Line separator, <400> field identifier  
L:2763 M:283 W: Missing Blank Line separator, <400> field identifier  
L:2879 M:283 W: Missing Blank Line separator, <220> field identifier  
L:2883 M:283 W: Missing Blank Line separator, <400> field identifier  
L:3059 M:283 W: Missing Blank Line separator, <400> field identifier  
L:3179 M:283 W: Missing Blank Line separator, <220> field identifier  
L:3182 M:283 W: Missing Blank Line separator, <400> field identifier  
L:3190 M:283 W: Missing Blank Line separator, <220> field identifier  
L:3193 M:283 W: Missing Blank Line separator, <400> field identifier

## SEQUENCE LISTING

<110> Kogel, Karl-Heinz  
 Huckelhoven, Ralph  
 Trujillo, Marco

<120> Method for Obtaining the pathogenic resistance in plants

<130> 12810-00067-US

<140> US 10/522,106  
 <141> 2005-01-24

<160> 24

<170> PatentIn version 3.3

<210> 1  
 <211> 337  
 <212> DNA  
 <213> Hordeum vulgare

<220>  
 <221> CDS  
 <222> (2)..(337)  
 <223> coding for NADPH oxidase (fragment)

<400> 1  
 g ttt aaa gga atc atg aat gag att gct gaa cta gat caa agg aat atc 49  
 Phe Lys Gly Ile Met Asn Glu Ile Ala Glu Leu Asp Gln Arg Asn Ile  
 1 5 10 15  
 att gag atg cac aac tat ctc aca agt gtt tat gag gaa ggg gat gct 97  
 Ile Glu Met His Asn Tyr Leu Thr Ser Val Tyr Glu Glu Gly Asp Ala  
 20 25 30  
 cgg tca gca ctc atc aca atg ctg caa gct ctc aac cat gcc aag aat 145  
 Arg Ser Ala Leu Ile Thr Met Leu Gln Ala Leu Asn His Ala Lys Asn  
 35 40 45  
 ggt gtc gat gta gtg tct ggm act cga gtc cgg aca cat ttt gca aga 193  
 Gly Val Asp Val Val Ser Xaa Thr Arg Val Arg Thr His Phe Ala Arg  
 50 55 60  
 cca aat ttt aag agg gtg ctg tct aag gta gcc gcc aaa cat cct tat 241  
 Pro Asn Phe Lys Arg Val Leu Ser Lys Val Ala Ala Lys His Pro Tyr  
 65 70 75 80  
 gcc aag ata gga gtg ttc tat tgc gga gct cca gtt ctg gcg cag gaa 289  
 Ala Lys Ile Gly Val Phe Tyr Cys Gly Ala Pro Val Leu Ala Gln Glu  
 85 90 95  
 cta agc aac ctt tgc cat gag ttc aat ggc aaa tgc acg aca aaa ttc 337  
 Leu Ser Asn Leu Cys His Glu Phe Asn Gly Lys Cys Thr Thr Lys Phe  
 100 105 110

<210> 2  
 <211> 112  
 <212> PRT  
 <213> Hordeum vulgare

<220>  
 <221> misc\_feature  
 <222> (55)..(55)  
 <223> The 'Xaa' at location 55 stands for Gly.

<400> 2  
 Phe Lys Gly Ile Met Asn Glu Ile Ala Glu Leu Asp Gln Arg Asn Ile



1				5					10					15	
Ile	Glu	Met	His	Asn	Tyr	Leu	Thr	Ser	Val	Tyr	Glu	Glu	Gly	Asp	Ala
			20					25					30		
Arg	Ser	Ala	Leu	Ile	Thr	Met	Leu	Gln	Ala	Leu	Asn	His	Ala	Lys	Asn
		35					40					45			
Gly	Val	Asp	Val	Val	Ser	Xaa	Thr	Arg	Val	Arg	Thr	His	Phe	Ala	Arg
	50				55				60						
Pro	Asn	Phe	Lys	Arg	Val	Leu	Ser	Lys	Val	Ala	Ala	Lys	His	Pro	Tyr
	65				70				75						80
Ala	Lys	Ile	Gly	Val	Phe	Tyr	Cys	Gly	Ala	Pro	Val	Leu	Ala	Gln	Glu
			85					90						95	
Leu	Ser	Asn	Leu	Cys	His	Glu	Phe	Asn	Gly	Lys	Cys	Thr	Thr	Lys	Phe
			100					105					110		

&lt;210&gt; 3

&lt;211&gt; 2832

&lt;212&gt; DNA

&lt;213&gt; Oryza sativa

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(2829)

&lt;223&gt; coding for NADPH oxidase

&lt;400&gt; 3

atg	agg	ggc	ggc	gcc	tcc	tcg	gga	ccc	cag	cga	tgg	ggc	tcg	gcg	ggg	48
Met	Arg	Gly	Gly	Ala	Ser	Ser	Gly	Pro	Gln	Arg	Trp	Gly	Ser	Ala	Gly	
1				5				10						15		
acg	aca	ccg	cgg	tcg	ctg	agc	acg	ggc	tcg	tcg	ccg	cgc	ggg	tcc	gac	96
Thr	Thr	Pro	Arg	Ser	Leu	Ser	Thr	Gly	Ser	Ser	Pro	Arg	Gly	Ser	Asp	
			20					25					30			
gac	cgg	agc	tcc	gac	gac	ggg	gag	gag	ctg	gtc	gag	gtc	acg	ctc	gac	144
Asp	Arg	Ser	Ser	Asp	Asp	Gly	Glu	Leu	Val	Glu	Val	Thr	Leu	Asp		
		35				40					45					
ctg	cag	gac	gac	gac	acc	att	gtg	ctt	cgg	agc	gtc	gag	ccc	gcg	gcg	192
Leu	Gln	Asp	Asp	Asp	Thr	Ile	Val	Leu	Arg	Ser	Val	Glu	Pro	Ala	Ala	
	50					55			60							
gcg	gcg	gcg	gcg	ggg	gtg	ggg	gcg	ggg	gcg	ggg	gcg	gcg	tcg	gcg	cgg	240
Ala	Ala	Ala	Ala	Gly	Val	Gly	Ala	Gly	Ala	Gly	Ala	Ala	Ser	Ala	Arg	
	65			70				75						80		
ggg	gag	ctc	acg	ggt	ggc	ccg	tcg	tcg	tcg	tcg	tcg	cgg	tcg	agg	tcg	288
Gly	Glu	Leu	Thr	Gly	Gly	Pro	Ser	Ser	Ser	Ser	Ser	Arg	Ser	Arg	Ser	
			85					90						95		
ccg	tcg	atc	cgg	agg	agc	tcg	tcg	cac	cgg	ctg	ctg	cag	ttc	tcg	cag	336
Pro	Ser	Ile	Arg	Arg	Ser	Ser	Ser	His	Arg	Leu	Leu	Gln	Phe	Ser	Gln	
			100					105					110			
gag	ctc	aag	gcg	gag	gcc	atg	gcc	cgg	gcg	cgg	cag	ttc	tcg	cag	gac	384
Glu	Leu	Lys	Ala	Glu	Ala	Met	Ala	Arg	Ala	Arg	Gln	Phe	Ser	Gln	Asp	
		115				120						125				
ctg	acc	aag	cgg	ttc	ggc	cgc	agc	cac	agc	cgc	agc	gaa	gcg	cag	gcg	432
Leu	Thr	Lys	Arg	Phe	Gly	Arg	Ser	His	Ser	Arg	Ser	Glu	Ala	Gln	Ala	
	130				135						140					
ccg	tcg	ggc	ctc	gag	tcc	gcg	ctc	gcc	gcc	cgc	gcc	gcg	cgg	cgg	cag	480
Pro	Ser	Gly	Leu	Glu	Ser	Ala	Leu	Ala	Ala	Arg	Ala	Ala	Arg	Arg	Gln	
	145				150					155				160		
cgc	gcg	cag	ctc	gac	cgc	aca	cgc	tcc	ggc	gcc	cac	aag	gcg	ctc	cgc	528
Arg	Ala	Gln	Leu	Asp	Arg	Thr	Arg	Ser	Gly	Ala	His	Lys	Ala	Leu	Arg	
			165					170					175			
ggc	ctc	cgc	ttc	atc	agc	agc	aac	aag	gcc	aac	aac	gcc	tgg	atg	gag	576
Gly	Leu	Arg	Phe	Ile	Ser	Ser	Asn	Lys	Ala	Asn	Asn	Ala	Trp	Met	Glu	
			180					185					190			

gtg	cag	gcc	aac	ttc	gac	cgc	ctc	gcc	cgc	gac	ggc	tac	ctc	tcc	cgc	624
Val	Gln	Ala	Asn	Phe	Asp	Arg	Leu	Ala	Arg	Asp	Gly	Tyr	Leu	Ser	Arg	
		195					200					205				
tcc	gac	ttc	gcc	gaa	tgc	atc	ggg	atg	acg	gaa	tcg	aag	gag	ttc	gcg	672
Ser	Asp	Phe	Ala	Glu	Cys	Ile	Gly	Met	Thr	Glu	Ser	Lys	Glu	Phe	Ala	
	210					215				220						
ctc	gag	ctg	ttc	gac	acg	ctg	agc	cgg	cga	cga	cag	atg	aag	gtg	gac	720
Leu	Glu	Leu	Phe	Asp	Thr	Leu	Ser	Arg	Arg	Arg	Gln	Met	Lys	Val	Asp	
225				230						235					240	
acg	att	aac	aag	gat	gaa	ctc	cgc	gag	atc	tgg	cag	cag	atc	acc	gat	768
Thr	Ile	Asn	Lys	Asp	Glu	Leu	Arg	Glu	Ile	Trp	Gln	Gln	Ile	Thr	Asp	
			245					250					255			
aac	agc	ttc	gac	tcc	cgt	ctc	caa	atc	ttc	ttc	gaa	atg	gtg	gat	aag	816
Asn	Ser	Phe	Asp	Ser	Arg	Leu	Gln	Ile	Phe	Phe	Glu	Met	Val	Asp	Lys	
		260					265					270				
aac	gcg	gac	ggc	cgg	att	acg	gag	gcg	gag	gtg	aaa	gag	att	att	atg	864
Asn	Ala	Asp	Gly	Arg	Ile	Thr	Glu	Ala	Glu	Val	Lys	Glu	Ile	Ile	Met	
	275						280				285					
ttg	agc	gcg	tct	gcc	aat	aaa	ctg	tcg	agg	ctt	aag	gag	caa	gca	gaa	912
Leu	Ser	Ala	Ser	Ala	Asn	Lys	Leu	Ser	Arg	Leu	Lys	Glu	Gln	Ala	Glu	
	290				295					300						
gag	tac	gcc	gct	ttg	atc	atg	gag	gag	ctt	gat	cct	gaa	ggg	ctc	ggc	960
Glu	Tyr	Ala	Ala	Leu	Ile	Met	Glu	Glu	Leu	Asp	Pro	Glu	Gly	Leu	Gly	
305				310					315						320	
tac	att	gag	cta	tgg	caa	ttg	gag	aca	ctt	ctg	ttg	cag	aaa	gat	acc	1008
Tyr	Ile	Glu	Leu	Trp	Gln	Leu	Glu	Thr	Leu	Leu	Leu	Gln	Lys	Asp	Thr	
			325					330						335		
tat	atg	aac	tat	agt	cag	gcc	ctt	agt	tac	aca	agc	caa	gca	ctg	agc	1056
Tyr	Met	Asn	Tyr	Ser	Gln	Ala	Leu	Ser	Tyr	Thr	Ser	Gln	Ala	Leu	Ser	
		340					345					350				
cag	aat	ctt	gca	ggg	cta	agg	aag	aag	agt	tca	atc	cgc	aaa	ata	agc	1104
Gln	Asn	Leu	Ala	Gly	Leu	Arg	Lys	Lys	Ser	Ser	Ile	Arg	Lys	Ile	Ser	
	355						360					365				
acc	tct	tta	agc	tac	tat	ttc	gag	gac	aac	tgg	aaa	cgt	tta	tgg	gtg	1152
Thr	Ser	Leu	Ser	Tyr	Tyr	Phe	Glu	Asp	Asn	Trp	Lys	Arg	Leu	Trp	Val	
	370					375				380						
ctt	gca	ttg	tgg	att	ggg	ata	atg	gct	gga	ctg	ttc	acc	tgg	aaa	ttc	1200
Leu	Ala	Leu	Trp	Ile	Gly	Ile	Met	Ala	Gly	Leu	Phe	Thr	Trp	Lys	Phe	
385				390					395						400	
atg	cag	tat	cgt	aac	cga	tat	gtc	ttt	gat	gtg	atg	ggc	tac	tgt	gtc	1248
Met	Gln	Tyr	Arg	Asn	Arg	Tyr	Val	Phe	Asp	Val	Met	Gly	Tyr	Cys	Val	
			405						410				415			
aca	aca	gca	aaa	gga	gct	gct	gaa	acc	cta	aag	ctg	aat	atg	gca	att	1296
Thr	Thr	Ala	Lys	Gly	Ala	Ala	Glu	Thr	Leu	Lys	Leu	Asn	Met	Ala	Ile	
		420					425					430				
atc	ctc	ctg	cca	gta	tgc	cgt	aac	acc	att	act	tgg	ttg	cga	agt	aca	1344
Ile	Leu	Leu	Pro	Val	Cys	Arg	Asn	Thr	Ile	Thr	Trp	Leu	Arg	Ser	Thr	
	435						440					445				
agg	gct	gca	cgg	gca	cta	cct	ttt	gat	gac	aac	atc	aac	ttc	cac	aag	1392
Arg	Ala	Ala	Arg	Ala	Leu	Pro	Phe	Asp	Asp	Asn	Ile	Asn	Phe	His	Lys	
	450					455				460						
act	att	gca	gca	gca	att	gtg	ggt	ata	atc	ctc	cat	gca	ggg	aac		1440
Thr	Ile	Ala	Ala	Ala	Ile	Val	Val	Gly	Ile	Ile	Leu	His	Ala	Gly	Asn	
465				470					475					480		
cac	ctt	gta	tgc	gat	ttt	cca	cgg	tta	ata	aaa	tca	tca	gat	gag	aag	1488
His	Leu	Val	Cys	Asp	Phe	Pro	Arg	Leu	Ile	Lys	Ser	Ser	Asp	Glu	Lys	
			485					490					495			
tat	gct	cct	ttg	ggc	cag	tat	ttt	ggg	gaa	ata	aag	cca	aca	tat	ttt	1536
Tyr	Ala	Pro	Leu	Gly	Gln	Tyr	Phe	Gly	Glu	Ile	Lys	Pro	Thr	Tyr	Phe	
		500						505					510			
aca	ttg	gtc	aaa	gga	gtg	gag	ggc	atc	act	ggg	gta	atc	atg	gtt	gta	1584

Thr	Leu	Val	Lys	Gly	Val	Glu	Gly	Ile	Thr	Gly	Val	Ile	Met	Val	Val	
		515					520					525				
tgc	atg	ata	att	gct	ttt	act	cta	gca	acc	cgg	tgg	ttc	cgc	cgt	agc	1632
Cys	Met	Ile	Ile	Ala	Phe	Thr	Leu	Ala	Thr	Arg	Trp	Phe	Arg	Arg	Ser	
		530					535					540				
ttg	gtt	aag	ctt	cca	agg	cca	ttt	gac	aaa	ctg	act	ggc	ttc	aat	gcc	1680
Leu	Val	Lys	Leu	Pro	Arg	Pro	Phe	Asp	Lys	Leu	Thr	Gly	Phe	Asn	Ala	
545						550				555					560	
ttt	tgg	tat	tct	cat	cat	ctg	ttc	atc	att	gtg	tat	atc	gcg	ctc	att	1728
Phe	Trp	Tyr	Ser	His	His	Leu	Phe	Ile	Ile	Val	Tyr	Ile	Ala	Leu	Ile	
				565					570					575		
gtt	cat	gga	gag	tgt	cta	tac	ctt	att	cat	gtc	tgg	tac	aga	aga	acg	1776
Val	His	Gly	Glu	Cys	Leu	Tyr	Leu	Ile	His	Val	Trp	Tyr	Arg	Arg	Thr	
			580					585					590			
aca	tgg	atg	tat	ctt	tca	gtg	cct	gtt	tgc	ttg	tat	gta	ggg	gag	agg	1824
Thr	Trp	Met	Tyr	Leu	Ser	Val	Pro	Val	Cys	Leu	Tyr	Val	Gly	Glu	Arg	
		595					600					605				
att	cta	agg	ttc	ttc	agg	tct	ggc	agt	tat	tct	gtc	cgg	cta	ttg	aag	1872
Ile	Leu	Arg	Phe	Phe	Arg	Ser	Gly	Ser	Tyr	Ser	Val	Arg	Leu	Leu	Lys	
	610					615					620					
gtg	gcc	ata	tat	cca	ggt	aat	gtt	ttg	aca	ctg	caa	atg	tcc	aag	cct	1920
Val	Ala	Ile	Tyr	Pro	Gly	Asn	Val	Leu	Thr	Leu	Gln	Met	Ser	Lys	Pro	
625					630					635					640	
ccc	acg	ttc	cgt	tac	aag	agt	gga	caa	tat	atg	ttt	gtt	caa	tgt	cca	1968
Pro	Thr	Phe	Arg	Tyr	Lys	Ser	Gly	Gln	Tyr	Met	Phe	Val	Gln	Cys	Pro	
				645					650					655		
gca	gtg	tct	ccc	ttt	gaa	tgg	cat	ccc	ttc	tca	att	act	tca	gca	cct	2016
Ala	Val	Ser	Pro	Phe	Glu	Trp	His	Pro	Phe	Ser	Ile	Thr	Ser	Ala	Pro	
			660					665					670			
ggg	gat	gac	tac	ctc	agc	att	cat	gtt	cga	caa	ctt	ggg	gat	tgg	aca	2064
Gly	Asp	Asp	Tyr	Leu	Ser	Ile	His	Val	Arg	Gln	Leu	Gly	Asp	Trp	Thr	
	675					680						685				
cga	gaa	ctc	aag	aga	gta	ttt	gct	gca	gct	tgt	gag	ccc	cca	gcg	ggg	2112
Arg	Glu	Leu	Lys	Arg	Val	Phe	Ala	Ala	Ala	Cys	Glu	Pro	Pro	Ala	Gly	
	690					695					700					
ggg	aaa	agc	ggc	ctt	ctt	agg	gca	gat	gag	aca	act	aag	aaa	atc	tta	2160
Gly	Lys	Ser	Gly	Leu	Leu	Arg	Ala	Asp	Glu	Thr	Thr	Lys	Lys	Ile	Leu	
705					710					715					720	
ccc	aag	ctt	ctg	att	gat	gga	ccg	tat	ggg	tct	cct	gct	cag	gat	tac	2208
Pro	Lys	Leu	Leu	Ile	Asp	Gly	Pro	Tyr	Gly	Ser	Pro	Ala	Gln	Asp	Tyr	
				725					730					735		
agc	aag	tat	gat	gtt	tta	tta	ctt	gtt	gga	tta	gga	att	ggg	gcg	aca	2256
Ser	Lys	Tyr	Asp	Val	Leu	Leu	Leu	Val	Gly	Leu	Gly	Ile	Gly	Ala	Thr	
			740					745					750			
ccc	ttt	att	agc	ata	tta	aaa	gat	ctt	ctg	aat	aac	atc	atc	aaa	atg	2304
Pro	Phe	Ile	Ser	Ile	Leu	Lys	Asp	Leu	Leu	Asn	Asn	Ile	Ile	Lys	Met	
		755					760					765				
gag	gaa	gag	gag	gat	gct	tct	act	gat	ctt	tat	cca	cca	atg	ggg	cgg	2352
Glu	Glu	Glu	Glu	Asp	Ala	Ser	Thr	Asp	Leu	Tyr	Pro	Pro	Met	Gly	Arg	
	770				775						780					
aat	aag	cca	cat	gtt	gat	ctg	ggc	aca	ctt	atg	acg	att	acc	tca	aga	2400
Asn	Lys	Pro	His	Val	Asp	Leu	Gly	Thr	Leu	Met	Thr	Ile	Thr	Ser	Arg	
	785				790					795					800	
cca	aag	aag	atc	ttg	aag	acc	aca	aat	gct	tac	ttt	tac	tgg	gtg	aca	2448
Pro	Lys	Lys	Ile	Leu	Lys	Thr	Thr	Asn	Ala	Tyr	Phe	Tyr	Trp	Val	Thr	
				805					810					815		
cgt	gag	caa	ggc	tct	ttt	gat	tgg	ttc	aaa	gga	gtc	atg	aat	gaa	att	2496
Arg	Glu	Gln	Gly	Ser	Phe	Asp	Trp	Phe	Lys	Gly	Val	Met	Asn	Glu	Ile	
			820					825					830			
gct	gac	ttg	gat	caa	agg	aat	atc	att	gag	atg	cac	aac	tac	cta	aca	2544
Ala	Asp	Leu	Asp	Gln	Arg	Asn	Ile	Ile	Glu	Met	His	Asn	Tyr	Leu	Thr	

835	840	845	
agc gtc tat gag gag ggg gat gcc agg tca gca ctc atc acc atg ctc			2592
Ser Val Tyr Glu Glu Gly Asp Ala Arg Ser Ala Leu Ile Thr Met Leu			
850	855	860	
caa gct ctg aac cat gcc aag aat gga gtt gat att gtc tct ggg aca			2640
Gln Ala Leu Asn His Ala Lys Asn Gly Val Asp Ile Val Ser Gly Thr			
865	870	875	880
aaa gtc cgg aca cat ttt gca cga cca aat tgg aga aag gtc ctt tct			2688
Lys Val Arg Thr His Phe Ala Arg Pro Asn Trp Arg Lys Val Leu Ser			
885	890	895	
aaa att tcc tcc aag cat cca tat gcc aaa ata ggt gta ttc tac tgt			2736
Lys Ile Ser Ser Lys His Pro Tyr Ala Lys Ile Gly Val Phe Tyr Cys			
900	905	910	
gga gct cca gtc ctg gca caa gaa cta agc aaa ctt tgc cat gaa ttc			2784
Gly Ala Pro Val Leu Ala Gln Glu Leu Ser Lys Leu Cys His Glu Phe			
915	920	925	
aac ggg aaa tgc aca acg aag ttc gaa ttc cat aag gag cat ttc tga			2832
Asn Gly Lys Cys Thr Thr Lys Phe Glu Phe His Lys Glu His Phe			
930	935	940	

&lt;210&gt; 4

&lt;211&gt; 943

&lt;212&gt; PRT

&lt;213&gt; Oryza sativa

&lt;400&gt; 4

Met Arg Gly Gly Ala Ser Ser Gly Pro Gln Arg Trp Gly Ser Ala Gly	
1 5 10 15	
Thr Thr Pro Arg Ser Leu Ser Thr Gly Ser Ser Pro Arg Gly Ser Asp	
20 25 30	
Asp Arg Ser Ser Asp Asp Gly Glu Glu Leu Val Glu Val Thr Leu Asp	
35 40 45	
Leu Gln Asp Asp Asp Thr Ile Val Leu Arg Ser Val Glu Pro Ala Ala	
50 55 60	
Ala Ala Ala Ala Gly Val Gly Ala Gly Ala Gly Ala Ser Ala Arg	
65 70 75 80	
Gly Glu Leu Thr Gly Gly Pro Ser Ser Ser Ser Ser Arg Ser Arg Ser	
85 90 95	
Pro Ser Ile Arg Arg Ser Ser Ser His Arg Leu Leu Gln Phe Ser Gln	
100 105 110	
Glu Leu Lys Ala Glu Ala Met Ala Arg Ala Arg Gln Phe Ser Gln Asp	
115 120 125	
Leu Thr Lys Arg Phe Gly Arg Ser His Ser Arg Ser Glu Ala Gln Ala	
130 135 140	
Pro Ser Gly Leu Glu Ser Ala Leu Ala Ala Arg Ala Ala Arg Arg Gln	
145 150 155 160	
Arg Ala Gln Leu Asp Arg Thr Arg Ser Gly Ala His Lys Ala Leu Arg	
165 170 175	
Gly Leu Arg Phe Ile Ser Ser Asn Lys Ala Asn Asn Ala Trp Met Glu	
180 185 190	
Val Gln Ala Asn Phe Asp Arg Leu Ala Arg Asp Gly Tyr Leu Ser Arg	
195 200 205	
Ser Asp Phe Ala Glu Cys Ile Gly Met Thr Glu Ser Lys Glu Phe Ala	
210 215 220	
Leu Glu Leu Phe Asp Thr Leu Ser Arg Arg Arg Gln Met Lys Val Asp	
225 230 235 240	
Thr Ile Asn Lys Asp Glu Leu Arg Glu Ile Trp Gln Gln Ile Thr Asp	
245 250 255	
Asn Ser Phe Asp Ser Arg Leu Gln Ile Phe Phe Glu Met Val Asp Lys	
260 265 270	
Asn Ala Asp Gly Arg Ile Thr Glu Ala Glu Val Lys Glu Ile Ile Met	

		275					280					285				
Leu	Ser	Ala	Ser	Ala	Asn	Lys	Leu	Ser	Arg	Leu	Lys	Glu	Gln	Ala	Glu	
	290					295					300					
Glu	Tyr	Ala	Ala	Leu	Ile	Met	Glu	Glu	Leu	Asp	Pro	Glu	Gly	Leu	Gly	
305					310					315					320	
Tyr	Ile	Glu	Leu	Trp	Gln	Leu	Glu	Thr	Leu	Leu	Leu	Gln	Lys	Asp	Thr	
				325					330					335		
Tyr	Met	Asn	Tyr	Ser	Gln	Ala	Leu	Ser	Tyr	Thr	Ser	Gln	Ala	Leu	Ser	
			340					345					350			
Gln	Asn	Leu	Ala	Gly	Leu	Arg	Lys	Lys	Ser	Ser	Ile	Arg	Lys	Ile	Ser	
		355					360					365				
Thr	Ser	Leu	Ser	Tyr	Tyr	Phe	Glu	Asp	Asn	Trp	Lys	Arg	Leu	Trp	Val	
	370					375					380					
Leu	Ala	Leu	Trp	Ile	Gly	Ile	Met	Ala	Gly	Leu	Phe	Thr	Trp	Lys	Phe	
385					390					395					400	
Met	Gln	Tyr	Arg	Asn	Arg	Tyr	Val	Phe	Asp	Val	Met	Gly	Tyr	Cys	Val	
				405					410					415		
Thr	Thr	Ala	Lys	Gly	Ala	Ala	Glu	Thr	Leu	Lys	Leu	Asn	Met	Ala	Ile	
			420					425					430			
Ile	Leu	Leu	Pro	Val	Cys	Arg	Asn	Thr	Ile	Thr	Trp	Leu	Arg	Ser	Thr	
		435					440					445				
Arg	Ala	Ala	Arg	Ala	Leu	Pro	Phe	Asp	Asp	Asn	Ile	Asn	Phe	His	Lys	
	450					455					460					
Thr	Ile	Ala	Ala	Ala	Ile	Val	Val	Gly	Ile	Ile	Leu	His	Ala	Gly	Asn	
465					470					475					480	
His	Leu	Val	Cys	Asp	Phe	Pro	Arg	Leu	Ile	Lys	Ser	Ser	Asp	Glu	Lys	
				485					490					495		
Tyr	Ala	Pro	Leu	Gly	Gln	Tyr	Phe	Gly	Glu	Ile	Lys	Pro	Thr	Tyr	Phe	
			500					505					510			
Thr	Leu	Val	Lys	Gly	Val	Glu	Gly	Ile	Thr	Gly	Val	Ile	Met	Val	Val	
		515					520					525				
Cys	Met	Ile	Ile	Ala	Phe	Thr	Leu	Ala	Thr	Arg	Trp	Phe	Arg	Arg	Ser	
	530					535					540					
Leu	Val	Lys	Leu	Pro	Arg	Pro	Phe	Asp	Lys	Leu	Thr	Gly	Phe	Asn	Ala	
545					550					555					560	
Phe	Trp	Tyr	Ser	His	His	Leu	Phe	Ile	Ile	Val	Tyr	Ile	Ala	Leu	Ile	
				565					570					575		
Val	His	Gly	Glu	Cys	Leu	Tyr	Leu	Ile	His	Val	Trp	Tyr	Arg	Arg	Thr	
			580					585					590			
Thr	Trp	Met	Tyr	Leu	Ser	Val	Pro	Val	Cys	Leu	Tyr	Val	Gly	Glu	Arg	
		595					600					605				
Ile	Leu	Arg	Phe	Phe	Arg	Ser	Gly	Ser	Tyr	Ser	Val	Arg	Leu	Leu	Lys	
	610					615					620					
Val	Ala	Ile	Tyr	Pro	Gly	Asn	Val	Leu	Thr	Leu	Gln	Met	Ser	Lys	Pro	
625					630											

Glu	Glu	Glu	Glu	Asp	Ala	Ser	Thr	Asp	Leu	Tyr	Pro	Pro	Met	Gly	Arg
770						775					780				
Asn	Lys	Pro	His	Val	Asp	Leu	Gly	Thr	Leu	Met	Thr	Ile	Thr	Ser	Arg
785					790					795					800
Pro	Lys	Lys	Ile	Leu	Lys	Thr	Thr	Asn	Ala	Tyr	Phe	Tyr	Trp	Val	Thr
				805					810					815	
Arg	Glu	Gln	Gly	Ser	Phe	Asp	Trp	Phe	Lys	Gly	Val	Met	Asn	Glu	Ile
			820					825					830		
Ala	Asp	Leu	Asp	Gln	Arg	Asn	Ile	Ile	Glu	Met	His	Asn	Tyr	Leu	Thr
		835					840					845			
Ser	Val	Tyr	Glu	Glu	Gly	Asp	Ala	Arg	Ser	Ala	Leu	Ile	Thr	Met	Leu
	850					855					860				
Gln	Ala	Leu	Asn	His	Ala	Lys	Asn	Gly	Val	Asp	Ile	Val	Ser	Gly	Thr
865					870					875					880
Lys	Val	Arg	Thr	His	Phe	Ala	Arg	Pro	Asn	Trp	Arg	Lys	Val	Leu	Ser
				885					890					895	
Lys	Ile	Ser	Ser	Lys	His	Pro	Tyr	Ala	Lys	Ile	Gly	Val	Phe	Tyr	Cys
			900					905					910		
Gly	Ala	Pro	Val	Leu	Ala	Gln	Glu	Leu	Ser	Lys	Leu	Cys	His	Glu	Phe
		915					920					925			
Asn	Gly	Lys	Cys	Thr	Thr	Lys	Phe	Glu	Phe	His	Lys	Glu	His	Phe	
	930					935					940				

&lt;210&gt; 5

&lt;211&gt; 2889

&lt;212&gt; DNA

&lt;213&gt; Nicotiana tabacum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(2886)

&lt;223&gt; coding for NADPH oxidase

&lt;400&gt; 5

atg	agg	ggg	tta	cct	ggg	cat	gaa	cgc	cgg	tgg	aca	tcc	gat	acg	gta	48
Met	Arg	Gly	Leu	Pro	Gly	His	Glu	Arg	Arg	Trp	Thr	Ser	Asp	Thr	Val	
1				5					10					15		
tct	tcc	gac	aag	gat	ttt	agt	ggg	gaa	tta	tcg	ccg	gga	gct	gat	tcc	96
Ser	Ser	Asp	Lys	Asp	Phe	Ser	Gly	Glu	Leu	Ser	Pro	Gly	Ala	Asp	Ser	
			20					25					30			
ggc	tat	aat	tcc	ggg	ttt	gct	tcc	gag	gag	ttt	gtt	gaa	gtc	acg	ctt	144
Gly	Tyr	Asn	Ser	Gly	Phe	Ala	Ser	Glu	Glu	Phe	Val	Glu	Val	Thr	Leu	
		35				40					45					
gat	ctt	cag	gat	gat	gat	acc	att	att	cta	cgg	agc	gtt	gaa	ccg	gct	192
Asp	Leu	Gln	Asp	Asp	Asp	Thr	Ile	Ile	Leu	Arg	Ser	Val	Glu	Pro	Ala	
	50					55				60						
act	gtg	att	aac	att	gac	gct	cct	gat	ctt	ccc	gcc	gga	gtc	ggg	att	240
Thr	Val	Ile	Asn	Ile	Asp	Ala	Pro	Asp	Leu	Pro	Ala	Gly	Val	Gly	Ile	
	65				70				75					80		
tcc	gga	gtt	tca	att	gaa	act	ccg	acg	tca	gca	tcg	gtg	tcg	gaa	tct	288
Ser	Gly	Val	Ser	Ile	Glu	Thr	Pro	Thr	Ser	Ala	Ser	Val	Ser	Glu	Ser	
				85					90					95		
cga	tcg	ccg	acg	atc	cgc	cgg	agt	tca	tct	agt	aaa	ctt	cgt	cag	ttt	336
Arg	Ser	Pro	Thr	Ile	Arg	Arg	Ser	Ser	Ser	Ser	Lys	Leu	Arg	Gln	Phe	
			100					105					110			
tca	cag	gag	ttg	aaa	gct	gag	gcg	gtt	gcg	aaa	gcg	agg	cag	ttt	tca	384
Ser	Gln	Glu	Leu	Lys	Ala	Glu	Ala	Val	Ala	Lys	Ala	Arg	Gln	Phe	Ser	
		115				120					125					
caa	gag	ctg	aag	gcg	gag	tta	agg	aga	ttc	tca	tgg	agc	cat	ggg	cat	432
Gln	Glu	Leu	Lys	Ala	Glu	Leu	Arg	Arg	Phe	Ser	Trp	Ser	His	Gly	His	
	130					135					140					

gcg	tct	cg	gcg	ttt	tcg	ccc	tcg	tcg	ttt	ttt	caa	aac	gcc	gtc	gtt	480
Ala	Ser	Arg	Ala	Phe	Ser	Pro	Ser	Ser	Phe	Phe	Gln	Asn	Ala	Val	Val	
145				150					155						160	
gga	aca	ggt	aac	ggc	gtg	gac	tcg	gct	tta	gcg	gca	cgt	gca	tta	cgt	528
Gly	Thr	Gly	Asn	Gly	Val	Asp	Ser	Ala	Leu	Ala	Ala	Arg	Ala	Leu	Arg	
				165					170						175	
cg	caa	cg	gcg	cag	ctt	gat	cg	act	cgt	tcc	agc	gcc	cat	aga	gct	576
Arg	Gln	Arg	Ala	Gln	Leu	Asp	Arg	Thr	Arg	Ser	Ser	Ala	His	Arg	Ala	
				180					185				190			
ctt	cgt	aga	ctc	aaa	ttc	att	agc	aat	aac	aaa	acc	aat	gga	tgg	aat	624
Leu	Arg	Arg	Leu	Lys	Phe	Ile	Ser	Asn	Asn	Lys	Thr	Asn	Gly	Trp	Asn	
				195				200				205				
gaa	gtt	gaa	aac	aat	ttc	tca	aag	ctc	gct	aaa	gac	ggt	tat	ctt	tac	672
Glu	Val	Glu	Asn	Asn	Phe	Ser	Lys	Leu	Ala	Lys	Asp	Gly	Tyr	Leu	Tyr	
	210						215					220				
cgt	tcc	gat	ttc	gca	caa	tgc	ata	ggt	atg	aag	gat	tcg	aag	gaa	ttt	720
Arg	Ser	Asp	Phe	Ala	Gln	Cys	Ile	Gly	Met	Lys	Asp	Ser	Lys	Glu	Phe	
					230					235					240	
gca	ttg	gaa	tta	ttt	gat	gct	ttg	agt	aga	aga	aga	aga	tta	aag	gtt	768
Ala	Leu	Glu	Leu	Phe	Asp	Ala	Leu	Ser	Arg	Arg	Arg	Arg	Leu	Lys	Val	
				245						250					255	
gat	aaa	att	agc	aag	gag	gaa	ttg	tat	gag	tac	tgg	tct	caa	atc	acc	816
Asp	Lys	Ile	Ser	Lys	Glu	Glu	Leu	Tyr	Glu	Tyr	Trp	Ser	Gln	Ile	Thr	
				260				265					270			
gat	cag	agt	ttc	gat	tct	cg	ctt	cag	atc	tcc	ttc	gac	atg	gtg	gac	864
Asp	Gln	Ser	Phe	Asp	Ser	Arg	Leu	Gln	Ile	Ser	Phe	Asp	Met	Val	Asp	
				275				280					285			
aag	aat	gaa	gat	ggt	cga	att	gct	gaa	gag	gaa	gta	aaa	gag	atc	atc	912
Lys	Asn	Glu	Asp	Gly	Arg	Ile	Ala	Glu	Glu	Glu	Val	Lys	Glu	Ile	Ile	
				290			295				300					
atg	cta	agt	gca	tct	gca	aac	aag	tta	tca	aga	tta	aaa	gaa	caa	gca	960
Met	Leu	Ser	Ala	Ser	Ala	Asn	Lys	Leu	Ser	Arg	Leu	Lys	Glu	Gln	Ala	
					310					315					320	
gag	gag	tat	gca	gct	tta	atc	atg	gaa	gaa	tta	gat	cct	gaa	aga	ctc	1008
Glu	Glu	Tyr	Ala	Ala	Leu	Ile	Met	Glu	Glu	Leu	Asp	Pro	Glu	Arg	Leu	
				325					330						335	
ggc	tac	att	gag	cta	tgg	cag	ctg	gaa	aca	ctt	ctc	ctc	caa	aag	gac	1056
Gly	Tyr	Ile	Glu	Leu	Trp	Gln	Leu	Glu	Thr	Leu	Leu	Leu	Gln	Lys	Asp	
				340					345						350	
act	tac	ctc	aac	tac	agt	caa	gca	cta	agt	tac	acg	agc	caa	gcc	ttg	1104
Thr	Tyr	Leu	Asn	Tyr	Ser	Gln	Ala	Leu	Ser	Tyr	Thr	Ser	Gln	Ala	Leu	
				355				360					365			
agc	caa	aac	ctt	cac	gga	tta	agg	aag	aaa	agc	cca	ata	aaa	aga	atg	1152
Ser	Gln	Asn	Leu	His	Gly	Leu	Arg	Lys	Lys	Ser	Pro	Ile	Lys	Arg	Met	
							375				380					
agc	aca	aaa	ctt	gtc	tat	tca	ttg	caa	gaa	aac	tgg	aag	aga	att	tgg	1200
Ser	Thr	Lys	Leu	Val	Tyr	Ser	Leu	Gln	Glu	Asn	Trp	Lys	Arg	Ile	Trp	
					390					395					400	
gtt	ctc	act	tta	tgg	att	ttg	ata	atg	att	ggg	ctt	ttt	ctt	tgg	aag	1248
Val	Leu	Thr	Leu	Trp	Ile	Leu	Ile	Met	Ile	Gly	Leu	Phe	Leu	Trp	Lys	
				405						410					415	
ttc	tat	cag	tac	aaa	aac	aag	agt	gca	ttc	cgt	gtc	atg	ggt	tat	tgc	1296
Phe	Tyr	Gln	Tyr	Lys	Asn	Lys	Ser	Ala	Phe	Arg	Val	Met	Gly	Tyr	Cys	
				420				425						430		
ctt	gtc	acg	gct	aag	ggc	gct	gct	gag	act	ctc	aag	ttc	aac	atg	gct	1344
Leu	Val	Thr	Ala	Lys	Gly	Ala	Ala	Glu	Thr	Leu	Lys	Phe	Asn	Met	Ala	
				435				440					445			
ctt	ata	tta	ttg	cca	gta	tgc	aga	aac	act	att	aca	tgg	ctc	agg	tcc	1392
Leu	Ile	Leu	Leu	Pro	Val	Cys	Arg	Asn	Thr	Ile	Thr	Trp	Leu	Arg	Ser	
				450			455				460					
acc	aag	ttg	agc	cat	ttt	gta	ccc	ttt	gac	gac	aac	atc	aac	ttt	cac	1440

Thr 465	Lys	Leu	Ser	His 470	Phe	Val	Pro	Phe	Asp 475	Asp	Asn	Ile	Asn	Phe	His 480	
aag	act	gtc	gct	gca	gcc	att	gtc	act	ggg	atc	ata	ctc	cat	gct	ggg	1488
Lys	Thr	Val	Ala	Ala	Ala	Ile	Val	Thr	Gly	Ile	Ile	Leu	His	Ala	Gly	
				485					490					495		
aac	cat	ctt	gta	tgt	gat	ttc	cca	agg	ctt	ata	cat	gca	gat	gat	caa	1536
Asn	His	Leu	Val	Cys	Asp	Phe	Pro	Arg	Leu	Ile	His	Ala	Asp	Asp	Gln	
			500					505				510				
gat	tat	caa	agt	ttt	ttg	tcg	aat	gat	ttt	ggc	caa	agt	aag	cct	gga	1584
Asp	Tyr	Gln	Ser	Phe	Leu	Ser	Asn	Asp	Phe	Gly	Gln	Ser	Lys	Pro	Gly	
		515					520				525					
tac	ata	gac	ctt	gtt	aaa	gga	gtt	gag	ggg	gtg	acg	gga	ata	ata	atg	1632
Tyr	Ile	Asp	Leu	Val	Lys	Gly	Val	Glu	Gly	Val	Thr	Gly	Ile	Ile	Met	
	530					535				540						
gta	atc	ctt	atg	gcc	att	gct	ttc	act	ctt	gct	aca	cga	tgg	ttt	aga	1680
Val	Ile	Leu	Met	Ala	Ile	Ala	Phe	Thr	Leu	Ala	Thr	Arg	Trp	Phe	Arg	
545					550					555					560	
cgg	agc	ctc	att	aag	ttg	ccc	aaa	cct	ttt	gat	aga	ctc	act	ggc	ttc	1728
Arg	Ser	Leu	Ile	Lys	Leu	Pro	Lys	Pro	Phe	Asp	Arg	Leu	Thr	Gly	Phe	
				565					570					575		
aat	gca	ttc	tgg	tat	tca	cac	cac	ctt	ctt	gtc	att	gtc	tac	atc	cta	1776
Asn	Ala	Phe	Trp	Tyr	Ser	His	His	Leu	Leu	Val	Ile	Val	Tyr	Ile	Leu	
			580					585				590				
ctg	atc	atc	cat	ggc	acg	ttc	ctc	ttc	ctt	gtg	cat	aaa	tgg	tac	tcc	1824
Leu	Ile	Ile	His	Gly	Thr	Phe	Leu	Phe	Leu	Val	His	Lys	Trp	Tyr	Ser	
		595					600					605				
aag	acg	acg	tgg	atg	tat	cta	gca	gtt	cct	gtg	ctt	ctc	tac	gca	ggg	1872
Lys	Thr	Thr	Trp	Met	Tyr	Leu	Ala	Val	Pro	Val	Leu	Leu	Tyr	Ala	Gly	
	610					615				620						
gaa	aga	act	ctt	aga	ttc	ttc	cgg	tca	ggc	ttg	tac	act	gtc	cgg	ctt	1920
Glu	Arg	Thr	Leu	Arg	Phe	Phe	Arg	Ser	Gly	Leu	Tyr	Thr	Val	Arg	Leu	
625					630					635					640	
ctg	aaa	gta	gca	ata	tat	cct	gga	aat	gtc	ctc	act	cta	caa	atg	tct	1968
Leu	Lys	Val	Ala	Ile	Tyr	Pro	Gly	Asn	Val	Leu	Thr	Leu	Gln	Met	Ser	
				645					650					655		
aag	cct	cct	caa	ttt	cga	tac	aaa	agt	gga	caa	tat	atg	ttt	gtc	cag	2016
Lys	Pro	Pro	Gln	Phe	Arg	Tyr	Lys	Ser	Gly	Gln	Tyr	Met	Phe	Val	Gln	
			660					665				670				
tgt	cca	gct	gtt	tct	cca	ttc	gag	tgg	cat	cca	ttt	tcc	att	act	tca	2064
Cys	Pro	Ala	Val	Ser	Pro	Phe	Glu	Trp	His	Pro	Phe	Ser	Ile	Thr	Ser	
		675					680					685				
gct	cct	ggg	gat	gac	tac	ttg	agc	att	cac	atc	cgg	caa	ctt	ggg	gac	2112
Ala	Pro	Gly	Asp	Asp	Tyr	Leu	Ser	Ile	His	Ile	Arg	Gln	Leu	Gly	Asp	
	690					695				700						
tgg	act	caa	gaa	ctc	aag	cgg	gtc	ttt	tct	gag	gct	tgc	gag	cgg	cca	2160
Trp	Thr	Gln	Glu	Leu	Lys	Arg	Val	Phe	Ser	Glu	Ala	Cys	Glu	Arg	Pro	
705					710					715					720	
gag	gct	gga	aag	agt	ggc	ctg	ctc	aga	gct	gac	gaa	aac	act	aag	aaa	2208
Glu	Ala	Gly	Lys	Ser	Gly	Leu	Leu	Arg	Ala	Asp	Glu	Asn	Thr	Lys	Lys	
				725					730					735		
agt	ttg	cca	aag	cta	tta	ata	gat	gga	cct	tac	gga	gct	cca	gca	caa	2256
Ser	Leu	Pro	Lys	Leu	Leu	Ile	Asp	Gly	Pro	Tyr	Gly	Ala	Pro	Ala	Gln	
		740						745				750				
gat	tac	cga	aaa	tat	gat	gtc	ttg	ctg	ctt	gtt	ggg	ctt	ggc	att	gga	2304
Asp	Tyr	Arg	Lys	Tyr	Asp	Val	Leu	Leu	Val	Gly	Leu	Gly	Ile	Gly		
		755				760						765				
gca	acg	cgg	ttc	ata	agt	atc	ctg	aaa	gac	ttg	ctc	gtt	aac	atc	gtg	2352
Ala	Thr	Pro	Phe	Ile	Ser	Ile	Leu	Lys	Asp	Leu	Leu	Val	Asn	Ile	Val	
	770					775						780				
aaa	atg	gag	gag	caa	gca	gat	tta	gcc	tca	gat	ttc	agt	ggg	aac	tca	2400
Lys	Met	Glu	Glu	Gln	Ala	Asp	Leu	Ala	Ser	Asp	Phe	Ser	Gly	Asn	Ser	



785		790		795		800	
gac atg agc gtt gcg aca agt gaa caa cca gct ctc aac aag att tct	2448						
Asp Met Ser Val Ala Thr Ser Glu Gln Pro Ala Leu Asn Lys Ile Ser							
805		810		815			
ctg aaa agg aga aag agc act cta aga acc aca aat gca tat ttt tat	2496						
Leu Lys Arg Arg Lys Ser Thr Leu Arg Thr Thr Asn Ala Tyr Phe Tyr							
820		825		830			
tgg gtg acc cgg gag caa gga tca ttt gat tgg ttc aaa ggc gtt atg	2544						
Trp Val Thr Arg Glu Gln Gly Ser Phe Asp Trp Phe Lys Gly Val Met							
835		840		845			
aac gaa gtg gct gaa ctt gat caa agg ggg gtc atc gag atg cat aac	2592						
Asn Glu Val Ala Glu Leu Asp Gln Arg Gly Val Ile Glu Met His Asn							
850		855		860			
tac ttg acg agt gtt tat gag gaa ggg gat gct cgt tca gct ctc att	2640						
Tyr Leu Thr Ser Val Tyr Glu Glu Gly Asp Ala Arg Ser Ala Leu Ile							
865		870		875		880	
acc atg gtc cag gca ctt aac cat gct aag aat ggg gtt gat att gta	2688						
Thr Met Val Gln Ala Leu Asn His Ala Lys Asn Gly Val Asp Ile Val							
885		890		895			
tca ggc acc agg gtg agg aca cat ttt gct agg cca aat tgg aag aaa	2736						
Ser Gly Thr Arg Val Arg Thr His Phe Ala Arg Pro Asn Trp Lys Lys							
900		905		910			
gta ttt tcc aag acc tta acc aag cat gca aat gca aga ata ggg gtt	2784						
Val Phe Ser Lys Thr Leu Thr Lys His Ala Asn Ala Arg Ile Gly Val							
915		920		925			
ttc tac tgt ggt gca ccc gta tta gca aaa gaa ctc agc aaa ctc tgc	2832						
Phe Tyr Cys Gly Ala Pro Val Leu Ala Lys Glu Leu Ser Lys Leu Cys							
930		935		940			
aaa gag tat aat caa aag ggt gca aca aag ttc gag ttt cac aaa gaa	2880						
Lys Glu Tyr Asn Gln Lys Gly Ala Thr Lys Phe Glu Phe His Lys Glu							
945		950		955		960	
cat ttt tag	2889						
His Phe							

&lt;210&gt; 6

&lt;211&gt; 962

&lt;212&gt; PRT

&lt;213&gt; Nicotiana tabacum

&lt;400&gt; 6

Met Arg Gly Leu Pro Gly His Glu Arg Arg Trp Thr Ser Asp Thr Val	
1 5 10 15	
Ser Ser Asp Lys Asp Phe Ser Gly Glu Leu Ser Pro Gly Ala Asp Ser	
20 25 30	
Gly Tyr Asn Ser Gly Phe Ala Ser Glu Glu Phe Val Glu Val Thr Leu	
35 40 45	
Asp Leu Gln Asp Asp Asp Thr Ile Ile Leu Arg Ser Val Glu Pro Ala	
50 55 60	
Thr Val Ile Asn Ile Asp Ala Pro Asp Leu Pro Ala Gly Val Gly Ile	
65 70 75 80	
Ser Gly Val Ser Ile Glu Thr Pro Thr Ser Ala Ser Val Ser Glu Ser	
85 90 95	
Arg Ser Pro Thr Ile Arg Arg Ser Ser Ser Lys Leu Arg Gln Phe	
100 105 110	
Ser Gln Glu Leu Lys Ala Glu Ala Val Ala Lys Ala Arg Gln Phe Ser	
115 120 125	
Gln Glu Leu Lys Ala Glu Leu Arg Arg Phe Ser Trp Ser His Gly His	
130 135 140	
Ala Ser Arg Ala Phe Ser Pro Ser Ser Phe Phe Gln Asn Ala Val Val	
145 150 155 160	
Gly Thr Gly Asn Gly Val Asp Ser Ala Leu Ala Ala Arg Ala Leu Arg	

				165					170					175	
Arg	Gln	Arg	Ala	Gln	Leu	Asp	Arg	Thr	Arg	Ser	Ser	Ala	His	Arg	Ala
			180					185					190		
Leu	Arg	Arg	Leu	Lys	Phe	Ile	Ser	Asn	Asn	Lys	Thr	Asn	Gly	Trp	Asn
		195					200					205			
Glu	Val	Glu	Asn	Asn	Phe	Ser	Lys	Leu	Ala	Lys	Asp	Gly	Tyr	Leu	Tyr
	210					215					220				
Arg	Ser	Asp	Phe	Ala	Gln	Cys	Ile	Gly	Met	Lys	Asp	Ser	Lys	Glu	Phe
225				230						235					240
Ala	Leu	Glu	Leu	Phe	Asp	Ala	Leu	Ser	Arg	Arg	Arg	Arg	Leu	Lys	Val
				245					250					255	
Asp	Lys	Ile	Ser	Lys	Glu	Glu	Leu	Tyr	Glu	Tyr	Trp	Ser	Gln	Ile	Thr
			260					265					270		
Asp	Gln	Ser	Phe	Asp	Ser	Arg	Leu	Gln	Ile	Ser	Phe	Asp	Met	Val	Asp
		275					280					285			
Lys	Asn	Glu	Asp	Gly	Arg	Ile	Ala	Glu	Glu	Glu	Val	Lys	Glu	Ile	Ile
	290					295					300				
Met	Leu	Ser	Ala	Ser	Ala	Asn	Lys	Leu	Ser	Arg	Leu	Lys	Glu	Gln	Ala
305					310					315					320
Glu	Glu	Tyr	Ala	Ala	Leu	Ile	Met	Glu	Glu	Leu	Asp	Pro	Glu	Arg	Leu
				325					330					335	
Gly	Tyr	Ile	Glu	Leu	Trp	Gln	Leu	Glu	Thr	Leu	Leu	Leu	Gln	Lys	Asp
			340					345					350		
Thr	Tyr	Leu	Asn	Tyr	Ser	Gln	Ala	Leu	Ser	Tyr	Thr	Ser	Gln	Ala	Leu
		355				360						365			
Ser	Gln	Asn	Leu	His	Gly	Leu	Arg	Lys	Lys	Ser	Pro	Ile	Lys	Arg	Met
	370					375					380				
Ser	Thr	Lys	Leu	Val	Tyr	Ser	Leu	Gln	Glu	Asn	Trp	Lys	Arg	Ile	Trp
385					390					395					400
Val	Leu	Thr	Leu	Trp	Ile	Leu	Ile	Met	Ile	Gly	Leu	Phe	Leu	Trp	Lys
				405					410					415	
Phe	Tyr	Gln	Tyr	Lys	Asn	Lys	Ser	Ala	Phe	Arg	Val	Met	Gly	Tyr	Cys
			420					425					430		
Leu	Val	Thr	Ala	Lys	Gly	Ala	Ala	Glu	Thr	Leu	Lys	Phe	Asn	Met	Ala
		435					440					445			
Leu	Ile	Leu	Leu	Pro	Val	Cys	Arg	Asn	Thr	Ile	Thr	Trp	Leu	Arg	Ser
	450					455					460				
Thr	Lys	Leu	Ser	His	Phe	Val	Pro	Phe	Asp	Asp	Asn	Ile	Asn	Phe	His
465					470					475					480
Lys	Thr	Val	Ala	Ala	Ala	Ile	Val	Thr	Gly	Ile	Ile	Leu	His	Ala	Gly
				485					490					495	
Asn	His	Leu	Val	Cys	Asp	Phe	Pro	Arg	Leu	Ile	His	Ala	Asp	Asp	Gln
			500					505					510		
Asp	Tyr	Gln	Ser	Phe	Leu	Ser	Asn	Asp	Phe	Gly	Gln	Ser	Lys	Pro	Gly

Lys Pro Pro Gln Phe Arg Tyr Lys Ser Gly Gln Tyr Met Phe Val Gln  
 660 665 670  
 Cys Pro Ala Val Ser Pro Phe Glu Trp His Pro Phe Ser Ile Thr Ser  
 675 680 685  
 Ala Pro Gly Asp Asp Tyr Leu Ser Ile His Ile Arg Gln Leu Gly Asp  
 690 695 700  
 Trp Thr Gln Glu Leu Lys Arg Val Phe Ser Glu Ala Cys Glu Arg Pro  
 705 710 715 720  
 Glu Ala Gly Lys Ser Gly Leu Leu Arg Ala Asp Glu Asn Thr Lys Lys  
 725 730 735  
 Ser Leu Pro Lys Leu Leu Ile Asp Gly Pro Tyr Gly Ala Pro Ala Gln  
 740 745 750  
 Asp Tyr Arg Lys Tyr Asp Val Leu Leu Val Gly Leu Gly Ile Gly  
 755 760 765  
 Ala Thr Pro Phe Ile Ser Ile Leu Lys Asp Leu Leu Val Asn Ile Val  
 770 775 780  
 Lys Met Glu Glu Gln Ala Asp Leu Ala Ser Asp Phe Ser Gly Asn Ser  
 785 790 795 800  
 Asp Met Ser Val Ala Thr Ser Glu Gln Pro Ala Leu Asn Lys Ile Ser  
 805 810 815  
 Leu Lys Arg Arg Lys Ser Thr Leu Arg Thr Thr Asn Ala Tyr Phe Tyr  
 820 825 830  
 Trp Val Thr Arg Glu Gln Gly Ser Phe Asp Trp Phe Lys Gly Val Met  
 835 840 845  
 Asn Glu Val Ala Glu Leu Asp Gln Arg Gly Val Ile Glu Met His Asn  
 850 855 860  
 Tyr Leu Thr Ser Val Tyr Glu Glu Gly Asp Ala Arg Ser Ala Leu Ile  
 865 870 875 880  
 Thr Met Val Gln Ala Leu Asn His Ala Lys Asn Gly Val Asp Ile Val  
 885 890 895  
 Ser Gly Thr Arg Val Arg Thr His Phe Ala Arg Pro Asn Trp Lys Lys  
 900 905 910  
 Val Phe Ser Lys Thr Leu Thr Lys His Ala Asn Ala Arg Ile Gly Val  
 915 920 925  
 Phe Tyr Cys Gly Ala Pro Val Leu Ala Lys Glu Leu Ser Lys Leu Cys  
 930 935 940  
 Lys Glu Tyr Asn Gln Lys Gly Ala Thr Lys Phe Glu Phe His Lys Glu  
 945 950 955 960  
 His Phe

&lt;210&gt; 7

&lt;211&gt; 3733

&lt;212&gt; DNA

&lt;213&gt; Solanum tuberosum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (92)..(2980)

&lt;223&gt; coding for NADPH oxidase

&lt;400&gt; 7

ggcacgagaa taacaaaaac ttttggtcag gcttctgcag aaaactctgt tttcaacata 60  
 tattttattta ttgtgctttg atttgggaca a atg agg ggt tta cct ggg cat 112  
 Met Arg Gly Leu Pro Gly His  
 1 5  
 gaa cgc cgg tgg acg tcg gat acg gta tct tcc ggc aag gat tta agt 160  
 Glu Arg Arg Trp Thr Ser Asp Thr Val Ser Ser Gly Lys Asp Leu Ser  
 10 15 20  
 ggt gag tca tcg ccg gga act gat tcc ggg aat att tcc ggt ttt gct 208  
 Gly Glu Ser Ser Pro Gly Thr Asp Ser Gly Asn Ile Ser Gly Phe Ala

25	30	35	
tcc gag gag ttt gtt gaa gtt ata ctt gat ctt cag gat gat gat acg			256
Ser Glu Glu Phe Val Glu Val Ile Leu Asp Leu Gln Asp Asp Asp Thr			
40	45	50	55
att att cta cgg agc gtt gaa ccg gct act gta atc aac att gat gct			304
Ile Ile Leu Arg Ser Val Glu Pro Ala Thr Val Ile Asn Ile Asp Ala			
	60	65	70
tct gat cct gct acc gga gtc ggt att ggt gga gta tcg att gaa act			352
Ser Asp Pro Ala Thr Gly Val Gly Ile Gly Gly Val Ser Ile Glu Thr			
	75	80	85
ccg gcg tcg ctg act tcg acg tcg gga act cga tcg ccg acg atg cgt			400
Pro Ala Ser Leu Thr Ser Thr Ser Gly Thr Arg Ser Pro Thr Met Arg			
	90	95	100
cgg agt aca tcg aat aaa tta cgt cag ttt tca cag gag ttg aaa gct			448
Arg Ser Thr Ser Asn Lys Leu Arg Gln Phe Ser Gln Glu Leu Lys Ala			
	105	110	115
gag gct gtc gcg aaa gcg aag cat ttc tcg caa gag ctt aaa gcg gag			496
Glu Ala Val Ala Lys Ala Lys His Phe Ser Gln Glu Leu Lys Ala Glu			
120	125	130	135
cta agg aga ttc tca tgg agc cat gga cat gcg tct cgc act ttt tcg			544
Leu Arg Arg Phe Ser Trp Ser His Gly His Ala Ser Arg Thr Phe Ser			
	140	145	150
ccg gcg tcg ttt ttc caa aac gcc gtc gtc ggt aca ggc aac ggt gta			592
Pro Ala Ser Phe Phe Gln Asn Ala Val Val Gly Thr Gly Asn Gly Val			
	155	160	165
gat tcg gct tta gca gct cga gca tta cga cgg cag cgc gct cag ctc			640
Asp Ser Ala Leu Ala Ala Arg Ala Leu Arg Arg Gln Arg Ala Gln Leu			
	170	175	180
gat cgg act cgt tcc agc gct cac aag gct ctt cgt gga ctc aaa ttc			688
Asp Arg Thr Arg Ser Ser Ala His Lys Ala Leu Arg Gly Leu Lys Phe			
	185	190	195
atc agc aat aac aaa act aac gga tgg aat gaa gtt gaa aac aat ttt			736
Ile Ser Asn Asn Lys Thr Asn Gly Trp Asn Glu Val Glu Asn Asn Phe			
200	205	210	215
gct aag ctc gct aaa gac ggt tac ctt tat cgc tcc gat ttc gca caa			784
Ala Lys Leu Ala Lys Asp Gly Tyr Leu Tyr Arg Ser Asp Phe Ala Gln			
	220	225	230
tgc atc ggt atg aag gat tca aag gaa ttt gca ttg gaa ttg ttt gat			832
Cys Ile Gly Met Lys Asp Ser Lys Glu Phe Ala Leu Glu Leu Phe Asp			
	235	240	245
gct ttg agt aga aga aga aga ttg aag gtt gat aag att agc aaa gag			880
Ala Leu Ser Arg Arg Arg Arg Leu Lys Val Asp Lys Ile Ser Lys Glu			
	250	255	260
gaa ttg tat gag tat tgg tct caa atc acc gat cag agt ttc gat tct			928
Glu Leu Tyr Glu Tyr Trp Ser Gln Ile Thr Asp Gln Ser Phe Asp Ser			
	265	270	275
cgg ctt cag atc ttc ttc gac atg gtg gac aag aat gaa gat ggt cga			976
Arg Leu Gln Ile Phe Phe Asp Met Val Asp Lys Asn Glu Asp Gly Arg			
280	285	290	295
att ggt gaa gaa gaa gta aaa gag atc atc atg cta agt gcc tct gca			1024
Ile Gly Glu Glu Glu Val Lys Glu Ile Ile Met Leu Ser Ala Ser Ala			
	300	305	310
aac aaa tta tca aga tta aaa gaa caa gca gag gag tat gca gct ctg			1072
Asn Lys Leu Ser Arg Leu Lys Glu Gln Ala Glu Glu Tyr Ala Ala Leu			
	315	320	325
atc atg gaa gaa tta gat cct gaa aga ctt ggc tac att gag cta tgg			1120
Ile Met Glu Glu Leu Asp Pro Glu Arg Leu Gly Tyr Ile Glu Leu Trp			
	330	335	340
cag ctg gaa acg ctt ctc ctc caa aag gac act tac ctc aac tac agt			1168
Gln Leu Glu Thr Leu Leu Leu Gln Lys Asp Thr Tyr Leu Asn Tyr Ser			
	345	350	355

caa gca cta agc tac aca agc caa gct ttg agc caa aac ctg caa ggg	1216
Gln Ala Leu Ser Tyr Thr Ser Gln Ala Leu Ser Gln Asn Leu Gln Gly	
360 365 370 375	
ttg agg aag aga agc cca ata aga aga atg agc aca aaa ctt gtc tat	1264
Leu Arg Lys Arg Ser Pro Ile Arg Arg Met Ser Thr Lys Leu Val Tyr	
380 385 390	
tca ctg caa gag aat tgg aag aga att tgg gtt ctg gtc ttg tgg att	1312
Ser Leu Gln Glu Asn Trp Lys Arg Ile Trp Val Leu Val Leu Trp Ile	
395 400 405	
ttg ata atg att gga ctt ttt ctt tgg aag ttc tat ctg tac aaa cag	1360
Leu Ile Met Ile Gly Leu Phe Leu Trp Lys Phe Tyr Leu Tyr Lys Gln	
410 415 420	
aaa agt gca ttt caa gtt atg ggt tat tgc ctt cta aca gct aag ggt	1408
Lys Ser Ala Phe Gln Val Met Gly Tyr Cys Leu Leu Thr Ala Lys Gly	
425 430 435	
gct gct gag act cta aag ttc aac atg gct ttg ata ttg ttg cca gtt	1456
Ala Ala Glu Thr Leu Lys Phe Asn Met Ala Leu Ile Leu Leu Pro Val	
440 445 450 455	
tgc agg aac acc att aca ttc ctc agg tct act aaa ttg agt tgt ttt	1504
Cys Arg Asn Thr Ile Thr Phe Leu Arg Ser Thr Lys Leu Ser Cys Phe	
460 465 470	
gta ccc ttt gat gac aac atc aac ttc cac aag act gtt gct gca gcc	1552
Val Pro Phe Asp Asp Asn Ile Asn Phe His Lys Thr Val Ala Ala Ala	
475 480 485	
att gtt act ggt atc ata ctc cat gcc ggt aat cat ctt gta tgt gat	1600
Ile Val Thr Gly Ile Ile Leu His Ala Gly Asn His Leu Val Cys Asp	
490 495 500	
ttc cca aag ctt ata cat gca aat aat acg aat tat cag aaa tat ttg	1648
Phe Pro Lys Leu Ile His Ala Asn Asn Thr Asn Tyr Gln Lys Tyr Leu	
505 510 515	
gtg aat gat ttt ggc cca agc cag cct cag tac ata gat ctt gtt aaa	1696
Val Asn Asp Phe Gly Pro Ser Gln Pro Gln Tyr Ile Asp Leu Val Lys	
520 525 530 535	
gga gtg gag ggt gtg aca gga ata ata atg gta atc ctc atg gcc att	1744
Gly Val Glu Gly Val Thr Gly Ile Ile Met Val Ile Leu Met Ala Ile	
540 545 550	
gct ttc act ctt gca acg cga tgg ttt agg cgg agc ctc att aag ttt	1792
Ala Phe Thr Leu Ala Thr Arg Trp Phe Arg Arg Ser Leu Ile Lys Phe	
555 560 565	
ccc aaa cct ttt gat aga ctc act ggt ttc aat gcg ttc tgg tac tcg	1840
Pro Lys Pro Phe Asp Arg Leu Thr Gly Phe Asn Ala Phe Trp Tyr Ser	
570 575 580	
cac cac ctt ctc atc att gtc tac atc gta ctg atc atc cat ggc aca	1888
His His Leu Leu Ile Ile Val Tyr Ile Val Leu Ile Ile His Gly Thr	
585 590 595	
ttc ctc tac ctt gtg cat aac tgg tac tcc aaa acg aca tgg atg tat	1936
Phe Leu Tyr Leu Val His Asn Trp Tyr Ser Lys Thr Thr Trp Met Tyr	
600 605 610 615	
cta gca gtt cct gta ctt ctc tac gca ggg gaa aga act ctt aga ttc	1984
Leu Ala Val Pro Val Leu Leu Tyr Ala Gly Glu Arg Thr Leu Arg Phe	
620 625 630	
ttc cga tca ggc tta tat aca gtc cgg ctt cta aaa gta gca ata tat	2032
Phe Arg Ser Gly Leu Tyr Thr Val Arg Leu Leu Lys Val Ala Ile Tyr	
635 640 645	
cct gga aat gtc ctt act ctg caa atg tct aag cct ccg caa ttt cga	2080
Pro Gly Asn Val Leu Thr Leu Gln Met Ser Lys Pro Pro Gln Phe Arg	
650 655 660	
tac aag agt gga caa tat atg ttt gtc cag tgt cca gct gtt tct cca	2128
Tyr Lys Ser Gly Gln Tyr Met Phe Val Gln Cys Pro Ala Val Ser Pro	
665 670 675	
ttc gag tgg cat cca ttt tcc att act tca gct cct ggg gat gac tac	2176

Phe 680	Glu	Trp	His	Pro	Phe 685	Ser	Ile	Thr	Ser	Ala 690	Pro	Gly	Asp	Asp	Tyr 695					
ttg	agc	att	cat	atc	cga	caa	ctt	ggc	gac	tgg	act	caa	gaa	ctc	aag	2224				
Leu	Ser	Ile	His	Ile 700	Arg	Gln	Leu	Gly	Asp 705	Trp	Thr	Gln	Glu	Leu	Lys					
cgg	gtg	ttt	tcc	gag	gct	tgc	gag	cag	cca	gag	gct	gga	aag	agt	ggc	2272				
Arg	Val	Phe	Ser	Glu 715	Ala	Cys	Glu	Gln	Pro 720	Glu	Ala	Gly	Lys	Ser	Gly					
ctg	ctc	aga	gct	gac	gaa	aac	acc	aaa	aca	agt	ttg	cca	aag	cta	ttg	2320				
Leu	Leu	Arg	Ala	Asp	Glu	Asn	Thr	Lys	Thr	Ser	Leu	Pro	Lys	Leu	Leu					
ata	gat	gga	cct	tat	gga	gct	cca	gca	caa	gat	tac	cga	aag	tat	gat	2368				
Ile	Asp	Gly	Pro	Tyr	Gly	Ala	Pro	Ala	Gln	Asp	Tyr	Arg	Lys	Tyr	Asp					
gtc	tta	ctg	ctt	gtt	ggc	ctt	ggc	att	gga	gca	act	ccc	ttt	ata	agt	2416				
Val	Leu	Leu	Leu	Val 760	Gly	Leu	Gly	Ile	Gly	Ala 770	Thr	Pro	Phe	Ile	Ser					
atc	ctg	aaa	gac	ttg	ctc	aaa	aac	atc	gtc	aca	atg	gag	gag	caa	gca	2464				
Ile	Leu	Lys	Asp	Leu 780	Leu	Lys	Asn	Ile	Val 785	Thr	Met	Glu	Glu	Gln	Ala					
gat	tta	gtc	tcg	gat	ttt	tca	ggg	aac	tca	gac	atg	agc	gct	gca	aca	2512				
Asp	Leu	Val	Ser	Asp 795	Phe	Ser	Gly	Asn	Ser 800	Asp	Met	Ser	Ala	Ala	Thr					
agt	gaa	caa	cca	gct	ctc	aac	aag	att	tct	cca	aaa	aag	aga	aag	agt	2560				
Ser	Glu	Gln	Pro	Ala	Leu	Asn	Lys	Ile	Ser	Pro	Lys	Lys	Arg	Lys	Ser					
act	cta	aaa	acc	aca	aat	gca	tat	ttt	tat	tgg	gtg	acc	cgg	gag	caa	2608				
Thr	Leu	Lys	Thr	Thr	Asn	Ala	Tyr	Phe	Tyr	Trp	Val	Thr	Arg	Glu	Gln					
gga	tca	ttt	gat	tgg	ttc	aaa	ggc	gtt	atg	aac	gaa	gtg	gct	gaa	ctt	2656				
Gly	Ser	Phe	Asp	Trp	Phe 840	Lys	Gly	Val	Met	Asn 850	Glu	Val	Ala	Glu	Leu					
gat	caa	agg	ggg	gtc	atc	gag	atg	cat	aac	tac	tta	acg	agt	gtt	tat	2704				
Asp	Gln	Arg	Gly	Val 860	Ile	Glu	Met	His	Asn 865	Tyr	Leu	Thr	Ser	Val	Tyr					
gag	gaa	ggg	gat	gca	cgt	tca	gct	ctc	att	acc	atg	gtc	cag	gcg	ctt	2752				
Glu	Glu	Gly	Asp	Ala 875	Arg	Ser	Ala	Leu	Ile 880	Thr	Met	Val	Gln	Ala	Leu					
aac	cat	gct	aag	aat	ggg	gtt	gat	att	gta	tca	ggc	acc	agt	gtg	agg	2800				
Asn	His	Ala	Lys	Asn	Gly	Val	Asp	Ile	Val	Ser	Gly	Thr	Ser	Val	Arg					
aca	cat	ttt	gcc	aga	ccg	aat	tgg	agg	aaa	gta	ttt	tcc	aag	acc	tta	2848				
Thr	His	Phe	Ala	Arg	Pro	Asn	Trp	Arg	Lys	Val	Phe	Ser	Lys	Thr	Leu					
acc	aag	cat	gca	aat	gca	aga	ata	gga	gtt	ttc	tac	tgc	ggc	gca	ccc	2896				
Thr	Lys	His	Ala	Asn	Ala 920	Arg	Ile	Gly	Val 930	Phe	Tyr	Cys	Gly	Ala	Pro					
ata	tta	gct	aaa	gaa	ctc	agc	aaa	ctc	tgc	aaa	gag	ttt	aac	caa	aag	2944				
Ile	Leu	Ala	Lys	Glu 940	Leu	Ser	Lys	Leu	Cys 945	Lys	Glu	Phe	Asn	Gln	Lys					
ggc	aca	acg	aag	ttc	gag	ttt	cac	aaa	gaa	cat	ttt	tagaaggccc				2990				
Gly	Thr	Thr	Lys 955	Phe	Glu	Phe	His	Lys 960	Glu	His	Phe									
tgga	gtac	aa	ttaat	ctt	gtc	atca	ac	ggta	cacac	atc	gg	taa	acc	agta	tttacc	cat	3050			
ctat	ctt	ttg	tac	ct	gatt	gat	gatt	ct	ctga	agac	at	aac	att	agta	agga	ata	ag	3110		
cagag	acaaa	ttgt	acata	aa	tagg	agga	ag	cacatt	tt	taca	gagaaa	ata	c	at	acca	at	at	3170		
gat	at	gt	gt	gta	tagg	ttt	gt	atatt	cag	tc	atct	gt	tat	c	ctt	caga	act	3230		
ccaaa	agg	gga	gact	ct	gct	tggt	ct	gat	g	ctt	aga	ata	tg	ggg	ag	gga	aaaa	agac	ga	3290
caatt	gaat	g	tcac	agata	c	acat	ga	agaa	tgaga	aat	att	tgga	aa	cag	c	gag	taata	aga	ag	3350
ttgac	ctt	ct	gtata	aa	gaa	acact	at	gaa	aat	gg	ca	agc	agata	aa	ggac	ag	caat	cat		3410
qgctt	ggat	q	gggaaa	acaa	aata	ca	at	ttt	tgaa	aga	aga	ata	at	att	ag	tagg	ag	ta		3470

```

gtgggggact gatagctttg ttggtggaac ttataatggg gctaagggaa tccttccaaa 3530
aaatgtctat gtagtaacta ctttttcttt tgctttgtga gtattttttg gggatatttta 3590
atatactact tattagataa gaggatagaa aatacgtgta tatgcaattc ttattagtaa 3650
agtttatctg tagtagttct ttaatctgga gaaaggtact atcaaaggaa atatctcatc 3710
gaaaaaaaaa aaaaaaaaaa aaa                                     3733

```

<210> 8

<211> 963

<212> PRT

<213> Solanum tuberosum

<400> 8

```

Met Arg Gly Leu Pro Gly His Glu Arg Arg Trp Thr Ser Asp Thr Val
 1          5          10          15
Ser Ser Gly Lys Asp Leu Ser Gly Glu Ser Ser Pro Gly Thr Asp Ser
 20          25          30
Gly Asn Ile Ser Gly Phe Ala Ser Glu Glu Phe Val Glu Val Ile Leu
 35          40          45
Asp Leu Gln Asp Asp Asp Thr Ile Ile Leu Arg Ser Val Glu Pro Ala
 50          55          60
Thr Val Ile Asn Ile Asp Ala Ser Asp Pro Ala Thr Gly Val Gly Ile
 65          70          75          80
Gly Gly Val Ser Ile Glu Thr Pro Ala Ser Leu Thr Ser Thr Ser Gly
 85          90          95
Thr Arg Ser Pro Thr Met Arg Arg Ser Thr Ser Asn Lys Leu Arg Gln
100          105          110
Phe Ser Gln Glu Leu Lys Ala Glu Ala Val Ala Lys Ala Lys His Phe
115          120          125
Ser Gln Glu Leu Lys Ala Glu Leu Arg Arg Phe Ser Trp Ser His Gly
130          135          140
His Ala Ser Arg Thr Phe Ser Pro Ala Ser Phe Phe Gln Asn Ala Val
145          150          155          160
Val Gly Thr Gly Asn Gly Val Asp Ser Ala Leu Ala Ala Arg Ala Leu
165          170          175
Arg Arg Gln Arg Ala Gln Leu Asp Arg Thr Arg Ser Ser Ala His Lys
180          185          190
Ala Leu Arg Gly Leu Lys Phe Ile Ser Asn Asn Lys Thr Asn Gly Trp
195          200          205
Asn Glu Val Glu Asn Asn Phe Ala Lys Leu Ala Lys Asp Gly Tyr Leu
210          215          220
Tyr Arg Ser Asp Phe Ala Gln Cys Ile Gly Met Lys Asp Ser Lys Glu
225          230          235          240
Phe Ala Leu Glu Leu Phe Asp Ala Leu Ser Arg Arg Arg Arg Leu Lys
245          250          255
Val Asp Lys Ile Ser Lys Glu Glu Leu Tyr Glu Tyr Trp Ser Gln Ile
260          265          270
Thr Asp Gln Ser Phe Asp Ser Arg Leu Gln Ile Phe Phe Asp Met Val
275          280          285
Asp Lys Asn Glu Asp Gly Arg Ile Gly Glu Glu Glu Val Lys Glu Ile
290          295          300
Ile Met Leu Ser Ala Ser Ala Asn Lys Leu Ser Arg Leu Lys Glu Gln
305          310          315          320
Ala Glu Glu Tyr Ala Ala Leu Ile Met Glu Glu Leu Asp Pro Glu Arg
325          330          335
Leu Gly Tyr Ile Glu Leu Trp Gln Leu Glu Thr Leu Leu Leu Gln Lys
340          345          350
Asp Thr Tyr Leu Asn Tyr Ser Gln Ala Leu Ser Tyr Thr Ser Gln Ala
355          360          365
Leu Ser Gln Asn Leu Gln Gly Leu Arg Lys Arg Ser Pro Ile Arg Arg
370          375          380
Met Ser Thr Lys Leu Val Tyr Ser Leu Gln Glu Asn Trp Lys Arg Ile

```

385					390					395				400
Trp	Val	Leu	Val	Leu	Trp	Ile	Leu	Ile	Met	Ile	Gly	Leu	Phe	Leu
				405					410					415
Lys	Phe	Tyr	Leu	Tyr	Lys	Gln	Lys	Ser	Ala	Phe	Gln	Val	Met	Gly
			420					425					430	
Cys	Leu	Leu	Thr	Ala	Lys	Gly	Ala	Ala	Glu	Thr	Leu	Lys	Phe	Asn
		435				440						445		
Ala	Leu	Ile	Leu	Leu	Pro	Val	Cys	Arg	Asn	Thr	Ile	Thr	Phe	Leu
	450					455					460			
Ser	Thr	Lys	Leu	Ser	Cys	Phe	Val	Pro	Phe	Asp	Asp	Asn	Ile	Asn
465					470					475				480
His	Lys	Thr	Val	Ala	Ala	Ala	Ile	Val	Thr	Gly	Ile	Ile	Leu	His
			485						490					495
Gly	Asn	His	Leu	Val	Cys	Asp	Phe	Pro	Lys	Leu	Ile	His	Ala	Asn
			500					505					510	
Thr	Asn	Tyr	Gln	Lys	Tyr	Leu	Val	Asn	Asp	Phe	Gly	Pro	Ser	Gln
		515				520						525		
Gln	Tyr	Ile	Asp	Leu	Val	Lys	Gly	Val	Glu	Gly	Val	Thr	Gly	Ile
	530					535					540			
Met	Val	Ile	Leu	Met	Ala	Ile	Ala	Phe	Thr	Leu	Ala	Thr	Arg	Trp
545					550					555				560
Arg	Arg	Ser	Leu	Ile	Lys	Phe	Pro	Lys	Pro	Phe	Asp	Arg	Leu	Thr
			565						570					575
Phe	Asn	Ala	Phe	Trp	Tyr	Ser	His	His	Leu	Leu	Ile	Ile	Val	Tyr
			580					585					590	
Val	Leu	Ile	Ile	His	Gly	Thr	Phe	Leu	Tyr	Leu	Val	His	Asn	Trp
		595				600						605		
Ser	Lys	Thr	Thr	Trp	Met	Tyr	Leu	Ala	Val	Pro	Val	Leu	Leu	Tyr
	610					615					620			
Gly	Glu	Arg	Thr	Leu	Arg	Phe	Phe	Arg	Ser	Gly	Leu	Tyr	Thr	Val
625					630					635				640
Leu	Leu	Lys	Val	Ala	Ile	Tyr	Pro	Gly	Asn	Val	Leu	Thr	Leu	Gln
			645						650					655
Ser	Lys	Pro	Pro	Gln	Phe	Arg	Tyr	Lys	Ser	Gly	Gln	Tyr	Met	Phe
			660					665					670	
Gln	Cys	Pro	Ala	Val	Ser	Pro	Phe	Glu	Trp	His	Pro	Phe	Ser	Ile
		675					680					685		
Ser	Ala	Pro	Gly	Asp	Asp	Tyr	Leu	Ser	Ile	His	Ile	Arg	Gln	Leu
	690					695					700			
Asp	Trp	Thr	Gln	Glu	Leu	Lys	Arg	Val	Phe	Ser	Glu	Ala	Cys	Glu
705					710					715				720
Pro	Glu	Ala	Gly	Lys	Ser	Gly	Leu	Leu	Arg	Ala	Asp	Glu	Asn	Thr
			725						730					735
Thr	Ser	Leu	Pro	Lys	Leu	Leu	Ile	Asp	Gly	Pro	Tyr	Gly	Ala	Pro
			740					745					750	
Gln	Asp	Tyr	Arg	Lys	Tyr	Asp	Val	Leu	Leu	Leu	Val	Gly	Leu	Gly
		755					760					765		
Gly	Ala	Thr	Pro	Phe	Ile	Ser	Ile	Leu	Lys	Asp	Leu	Leu	Lys	Asn
	770					775					780			
Val	Thr	Met	Glu	Glu	Gln	Ala	Asp	Leu	Val	Ser	Asp	Phe	Ser	Gly
785					790					795				800
Ser	Asp	Met	Ser	Ala	Ala	Thr	Ser	Glu	Gln	Pro	Ala	Leu	Asn	Lys
				805						810				815
Ser	Pro	Lys	Lys	Arg	Lys	Ser	Thr	Leu	Lys	Thr	Thr	Asn	Ala	Tyr
			820					825					830	
Tyr	Trp	Val	Thr	Arg	Glu	Gln	Gly	Ser	Phe	Asp	Trp	Phe	Lys	Gly
		835					840					845		
Met	Asn	Glu	Val	Ala	Glu	Leu	Asp	Gln	Arg	Gly	Val	Ile	Glu	Met
	850					855					860			
Asn	Tyr	Leu	Thr	Ser	Val	Tyr	Glu	Glu	Gly	Asp	Ala	Arg	Ser	Ala
865					870					875				880



```

Ile Thr Met Val Gln Ala Leu Asn His Ala Lys Asn Gly Val Asp Ile
                        885                        890                        895
Val Ser Gly Thr Ser Val Arg Thr His Phe Ala Arg Pro Asn Trp Arg
                        900                        905                        910
Lys Val Phe Ser Lys Thr Leu Thr Lys His Ala Asn Ala Arg Ile Gly
                        915                        920                        925
Val Phe Tyr Cys Gly Ala Pro Ile Leu Ala Lys Glu Leu Ser Lys Leu
                        930                        935                        940
Cys Lys Glu Phe Asn Gln Lys Gly Thr Thr Lys Phe Glu Phe His Lys
945                        950                        955                        960
Glu His Phe

```

```

<210> 9
<211> 3316
<212> DNA
<213> Lycopersicon esculentum

<220>
<221> CDS
<222> (146)..(3112)
<223> coding for NADPH oxidase

```

```

<400> 9
cgccactcgt gccgaattcg gcacgaggct ctgaaaaact tttcatacaa agccaatcta 60
tttctctctc tttcttttgg tcaggcttct acagaaaact ctgttttcaa cgtatattta 120
tttattgtca tttgatttgg gacag atg agg ggt tta cct ggg cat gaa cgc 172
                        Met Arg Gly Leu Pro Gly His Glu Arg
                        1                        5

cgg tgg acg tcg gat acg gtg tct tcc ggg aag gat tta agt ggt gag 220
Arg Trp Thr Ser Asp Thr Val Ser Ser Gly Lys Asp Leu Ser Gly Glu
10                        15                        20                        25

tca tcg ccg gga act gat tcc ggg aat att tcc ggt ttt gct tcg gag 268
Ser Ser Pro Gly Thr Asp Ser Gly Asn Ile Ser Gly Phe Ala Ser Glu
30                        35                        40

gag ttt gtt gaa gtt ata ctt gat ctt cag gat gat gat acg att att 316
Glu Phe Val Glu Val Ile Leu Asp Leu Gln Asp Asp Asp Thr Ile Ile
45                        50                        55

tta cgg agc gtt gaa ccg gct act gta atc aac att gat ggt tct gat 364
Leu Arg Ser Val Glu Pro Ala Thr Val Ile Asn Ile Asp Gly Ser Asp
60                        65                        70

cct gct tcc gga gtc ggt att ggt gga gca tcg att gaa act ccg gcg 412
Pro Ala Ser Gly Val Gly Ile Gly Gly Ala Ser Ile Glu Thr Pro Ala
75                        80                        85

tcg gtg acg tcg acg tcg gaa act cga tcg ccg atg atg cgt ccg agt 460
Ser Val Thr Ser Thr Ser Glu Thr Arg Ser Pro Met Met Arg Arg Ser
90                        95                        100                        105

aca tct aat aag ttt cgt cag ttt tca cag gag ttg aaa gct gag gct 508
Thr Ser Asn Lys Phe Arg Gln Phe Ser Gln Glu Leu Lys Ala Glu Ala
110                        115                        120

gtt gcg aaa gcg aag cat ttc tcg caa gag ctt aaa gcg gag cta agg 556
Val Ala Lys Ala Lys His Phe Ser Gln Glu Leu Lys Ala Glu Leu Arg
125                        130                        135

aga ttc tca tgg agc cat gga cat gcg tct cgt gct ttt tcg ccg gcg 604
Arg Phe Ser Trp Ser His Gly His Ala Ser Arg Ala Phe Ser Pro Ala
140                        145                        150

tcg ttt ttc caa aac gct gtc gtc gga aca ggc aac ggt gta gac tcg 652
Ser Phe Phe Gln Asn Ala Val Val Gly Thr Gly Asn Gly Val Asp Ser
155                        160                        165

gct tta gcg gct cga gca tta cgt cgg cag cgt gct cag ctc gac ccg 700
Ala Leu Ala Ala Arg Ala Leu Arg Arg Gln Arg Ala Gln Leu Asp Arg

```

170	act	cgt	tcc	agc	gca	cac	aag	gct	ctt	cgt	gga	ctc	aaa	ttc	atc	agc	748
	Thr	Arg	Ser	Ser	Ala	His	Lys	Ala	Leu	Arg	Gly	Leu	Lys	Phe	Ile	Ser	
					190					195					200		
	aat	aac	aaa	act	aac	gga	tgg	aat	gaa	ggt	gaa	aac	aat	ttc	gct	aag	796
	Asn	Asn	Lys	Thr	Asn	Gly	Trp	Asn	Glu	Val	Glu	Asn	Asn	Phe	Ala	Lys	
				205					210					215			
	ctc	gct	aaa	gac	ggt	tac	ctt	tat	cgt	tcc	gat	ttc	gca	caa	tgc	atc	844
	Leu	Ala	Lys	Asp	Gly	Tyr	Leu	Tyr	Arg	Ser	Asp	Phe	Ala	Gln	Cys	Ile	
				220					225				230				
	ggt	cag	tac	tca	cgc	cgg	cga	tca	cta	cag	ttt	aat	tat	aga	tta	att	892
	Gly	Gln	Tyr	Ser	Arg	Arg	Arg	Ser	Leu	Gln	Phe	Asn	Tyr	Arg	Leu	Ile	
		235					240					245					
	aca	tta	att	ttg	att	aat	tat	ttg	ggt	aaa	ggt	atg	aag	gat	tca	aag	940
	Thr	Leu	Ile	Leu	Ile	Asn	Tyr	Leu	Val	Lys	Gly	Met	Lys	Asp	Ser	Lys	
	250					255				260					265		
	gaa	ttt	gcg	ttg	gaa	ttg	ttt	gat	gct	tta	agt	aga	aga	aga	aga	ttg	988
	Glu	Phe	Ala	Leu	Glu	Leu	Phe	Asp	Ala	Leu	Ser	Arg	Arg	Arg	Arg	Leu	
					270				275						280		
	aag	ggt	gat	aag	att	agc	caa	gag	gaa	ttg	tat	gag	tat	tgg	tct	caa	1036
	Lys	Val	Asp	Lys	Ile	Ser	Gln	Glu	Glu	Leu	Tyr	Glu	Tyr	Trp	Ser	Gln	
				285					290					295			
	atc	acc	gat	cag	agt	ttc	gat	tct	cgg	ctt	cag	atc	ttc	ttc	gac	atg	1084
	Ile	Thr	Asp	Gln	Ser	Phe	Asp	Ser	Arg	Leu	Gln	Ile	Phe	Phe	Asp	Met	
				300				305					310				
	gtg	gac	aag	aat	gaa	gat	ggt	cga	att	ggt	gaa	gaa	gaa	gta	aaa	gag	1132
	Val	Asp	Lys	Asn	Glu	Asp	Gly	Arg	Ile	Gly	Glu	Glu	Glu	Val	Lys	Glu	
		315					320					325					
	atc	atc	atg	cta	agt	gcc	tct	gca	aac	aaa	tta	tca	aga	tta	aaa	gaa	1180
	Ile	Ile	Met	Leu	Ser	Ala	Ser	Ala	Asn	Lys	Leu	Ser	Arg	Leu	Lys	Glu	
	330					335					340					345	
	caa	gca	gag	gag	tat	gca	gct	ctg	atc	atg	gaa	gaa	tta	gat	cct	gaa	1228
	Gln	Ala	Glu	Glu	Tyr	Ala	Ala	Leu	Ile	Met	Glu	Glu	Leu	Asp	Pro	Glu	
					350					355					360		
	aga	ctt	ggc	tac	att	gag	cta	tgg	cag	ctg	gaa	aca	ctt	ctc	ctc	caa	1276
	Arg	Leu	Gly	Tyr	Ile	Glu	Leu	Trp	Gln	Leu	Glu	Thr	Leu	Leu	Leu	Gln	
				365					370					375			
	aag	gac	act	tac	ctc	aac	tac	agt	caa	gca	cta	agc	tac	aca	agc	caa	1324
	Lys	Asp	Thr	Tyr	Leu	Asn	Tyr	Ser	Gln	Ala	Leu	Ser	Tyr	Thr	Ser	Gln	
				380				385					390				
	gct	ttg	agc	caa	aat	ctg	caa	ggg	ttg	agg	aag	aga	agc	cca	ata	aga	1372
	Ala	Leu	Ser	Gln	Asn	Leu	Gln	Gly	Leu	Arg	Lys	Arg	Ser	Pro	Ile	Arg	
		395					400					405					
	aga	atg	agc	aca	aaa	ctt	gtc	tat	tca	ctg	caa	gag	aat	tgg	aag	aga	1420
	Arg	Met	Ser	Thr	Lys	Leu	Val	Tyr	Ser	Leu	Gln	Glu	Asn	Trp	Lys	Arg	
	410					415					420				425		
	att	tgg	ggt	ctg	gtc	ttg	tgg	att	ttg	ata	atg	att	gga	ctt	ttt	ctt	1468
	Ile	Trp	Val	Leu	Val	Leu	Trp	Ile	Leu	Ile	Met	Ile	Gly	Leu	Phe	Leu	
					430					435					440		
	tgg	aag	ttc	tat	cag	tac	aaa	cag	aaa	agt	gca	ttt	caa	gtc	atg	ggt	1516
	Trp	Lys	Phe	Tyr	Gln	Tyr	Lys	Gln	Lys	Ser	Ala	Phe	Gln	Val	Met	Gly	
				445					450					455			
	tat	tgc	ctt	cta	aca	gct	aag	ggt	gct	gct	gag	act	ctc	aag	ttc	aac	1564
	Tyr	Cys	Leu	Thr	Ala	Lys	Gly	Ala	Ala	Glu	Thr		Leu	Lys	Phe	Asn	
			460					465					470				
	atg	gct	tta	ata	ttg	ttg	cca	gta	tgc	agg	aac	acc	att	aca	ttc	ctc	1612
	Met	Ala	Leu	Ile	Leu	Leu	Pro	Val	Cys	Arg	Asn	Thr	Ile	Thr	Phe	Leu	
		475					480					485					
	agg	tct	act	aaa	ttg	agc	tgt	ttt	gta	ccc	ttt	gat	gac	aac	ata	aac	1660
	Arg	Ser	Thr	Lys	Leu	Ser	Cys	Phe	Val	Pro	Phe	Asp	Asp	Asn	Ile	Asn	
	490					495					500					505	

ttt	cac	aag	act	gtt	gct	gca	gcc	att	gtc	act	ggg	atc	ata	ctc	cat	1708
Phe	His	Lys	Thr	Val	Ala	Ala	Ala	Ile	Val	Thr	Gly	Ile	Ile	Leu	His	
			510						515					520		
gcc	ggg	aat	cac	ctt	gta	tgt	gat	ttc	cca	aag	ctt	ata	cat	gca	aat	1756
Ala	Gly	Asn	His	Leu	Val	Cys	Asp	Phe	Pro	Lys	Leu	Ile	His	Ala	Asn	
			525					530						535		
agt	acg	aat	tat	cag	aaa	tat	ttg	gtg	aat	gat	ttt	ggc	cca	agc	cag	1804
Ser	Thr	Asn	Tyr	Gln	Lys	Tyr	Leu	Val	Asn	Asp	Phe	Gly	Pro	Ser	Gln	
			540				545					550				
cct	cag	tac	ata	gat	ctt	gtt	aaa	gga	gtg	gag	ggg	gtg	act	gga	ata	1852
Pro	Gln	Tyr	Ile	Asp	Leu	Val	Lys	Gly	Val	Glu	Gly	Val	Thr	Gly	Ile	
			555			560					565					
gtt	atg	gta	atc	ctc	atg	gcc	att	gct	ttc	act	ctt	gca	acg	cga	tgg	1900
Val	Met	Val	Ile	Leu	Met	Ala	Ile	Ala	Phe	Thr	Leu	Ala	Thr	Arg	Trp	
					575					580					585	
ttt	agg	cgg	agc	ctc	att	aag	tta	ccc	aaa	cct	ttt	gat	aga	ctc	act	1948
Phe	Arg	Arg	Ser	Leu	Ile	Lys	Leu	Pro	Lys	Pro	Phe	Asp	Arg	Leu	Thr	
			590					595						600		
ggg	ttc	aat	gcg	ttc	tgg	tac	tcg	cac	cac	ctt	ctc	atc	att	gtc	tac	1996
Gly	Phe	Asn	Ala	Phe	Trp	Tyr	Ser	His	His	Leu	Leu	Ile	Ile	Val	Tyr	
			605					610						615		
atc	gta	ctg	atc	atc	cat	ggc	aca	ttc	ctc	tac	ctt	gtg	cat	aac	tgg	2044
Ile	Val	Leu	Ile	Ile	His	Gly	Thr	Phe	Leu	Tyr	Leu	Val	His	Asn	Trp	
			620			625						630				
tac	tcc	aaa	acg	aca	tgg	atg	tat	ata	gca	gtt	cct	gta	ctt	ctt	tac	2092
Tyr	Ser	Lys	Thr	Thr	Trp	Met	Tyr	Ile	Ala	Val	Pro	Val	Leu	Leu	Tyr	
			635			640					645					
gca	ggg	gaa	aga	act	ctt	aga	ttc	ttc	cga	tca	ggc	tta	tac	agt	gtc	2140
Ala	Gly	Glu	Arg	Thr	Leu	Arg	Phe	Phe	Arg	Ser	Gly	Leu	Tyr	Ser	Val	
					655					660					665	
cgg	ctt	cta	aaa	gta	gca	ata	tat	cct	gga	aat	gtc	ctt	act	ctg	caa	2188
Arg	Leu	Leu	Lys	Val	Ala	Ile	Tyr	Pro	Gly	Asn	Val	Leu	Thr	Leu	Gln	
			670					675						680		
atg	tct	aag	cct	ccg	caa	ttt	cga	tac	aag	agt	gga	cag	tat	atg	ttt	2236
Met	Ser	Lys	Pro	Pro	Gln	Phe	Arg	Tyr	Lys	Ser	Gly	Gln	Tyr	Met	Phe	
			685					690						695		
gtc	cag	tgt	cca	gct	gtt	tct	cca	ttc	gag	tgg	cat	cca	ttt	tcc	att	2284
Val	Gln	Cys	Pro	Ala	Val	Ser	Pro	Phe	Glu	Trp	His	Pro	Phe	Ser	Ile	
			700				705					710				
act	tca	gct	cct	ggg	gat	gac	tac	ttg	agc	att	cat	atc	cga	caa	ctt	2332
Thr	Ser	Ala	Pro	Gly	Asp	Asp	Tyr	Leu	Ser	Ile	His	Ile	Arg	Gln	Leu	
			715			720					725					
ggg	gac	tgg	act	caa	gaa	ctc	aag	cga	gtg	ttt	tcc	gag	gct	tgc	gag	2380
Gly	Asp	Trp	Thr	Gln	Glu	Leu	Lys	Arg	Val	Phe	Ser	Glu	Ala	Cys	Glu	
			730			735				740					745	
cag	cca	gag	gct	gga	aag	agt	ggc	ctg	ctc	aga	gct	gac	gaa	aac	acc	2428
Gln	Pro	Glu	Ala	Gly	Lys	Ser	Gly	Leu	Leu	Arg	Ala	Asp	Glu	Asn	Thr	
			750					755						760		
aaa	aca	agt	ttg	cca	aag	cta	tta	ata	gat	gga	cct	tat	gga	gct	cca	2476
Lys	Thr	Ser	Leu	Pro	Lys	Leu	Leu	Ile	Asp	Gly	Pro	Tyr	Gly	Ala	Pro	
			765					770						775		
gca	caa	gat	tac	cgg	aag	tat	gat	gtc	tta	ctg	ctt	gtt	ggg	ctt	ggc	2524
Ala	Gln	Asp	Tyr	Arg	Lys	Tyr	Asp	Val	Leu	Leu	Leu	Val	Gly	Leu	Gly	
			780				785					790				
att	gga	gca	act	ccc	ttt	ata	agt	atc	ctg	aaa	gac	ttg	ctc	aaa	aac	2572
Ile	Gly	Ala	Thr	Pro	Phe	Ile	Ser	Ile	Leu	Lys	Asp	Leu	Leu	Lys	Asn	
			795			800					805					
atc	gtc	gca	atg	gag	gag	caa	gca	gat	tta	gtc	tcg	gat	ttc	agt	gga	2620
Ile	Val	Ala	Met	Glu	Glu	Gln	Ala	Asp	Leu	Val	Ser	Asp	Phe	Ser	Gly	
			810			815				820					825	
aac	tcg	gac	atg	agt	gct	gca	aca	agt	gaa	caa	cca	gct	ctc	aac	aag	2668

Asn	Ser	Asp	Met	Ser	Ala	Ala	Thr	Ser	Glu	Gln	Pro	Ala	Leu	Asn	Lys	
				830					835					840		
att	tct	cca	aaa	aag	aga	aag	agt	act	cta	aaa	acc	aca	aat	gca	tat	2716
Ile	Ser	Pro	Lys	Lys	Arg	Lys	Ser	Thr	Leu	Lys	Thr	Thr	Asn	Ala	Tyr	
			845					850					855			
ttt	tat	tggtg	acc	cgg	gag	caa	gga	tca	ttt	gat	tggttc	aaa	ggt		2764	
Phe	Tyr	Trp	Val	Thr	Arg	Glu	Gln	Gly	Ser	Phe	Asp	Trp	Phe	Lys	Gly	
		860					865				870					
gtt	atg	aata	gaa	gtg	gct	gaa	ctt	gat	caa	agg	ggt	gtc	atc	gag	atg	2812
Val	Met	Asn	Glu	Val	Ala	Glu	Leu	Asp	Gln	Arg	Gly	Val	Ile	Glu	Met	
	875					880			885							
cat	aac	tac	ttg	acg	agt	gtt	tat	gag	gaa	ggg	gat	gca	cgt	tca	gct	2860
His	Asn	Tyr	Leu	Thr	Ser	Val	Tyr	Glu	Glu	Gly	Asp	Ala	Arg	Ser	Ala	
	890				895				900					905		
ctc	att	acc	atg	gtc	cag	gca	ctt	aac	cat	gct	aag	aat	ggg	gtt	gat	2908
Leu	Ile	Thr	Met	Val	Gln	Ala	Leu	Asn	His	Ala	Lys	Asn	Gly	Val	Asp	
			910					915					920			
att	gta	tca	ggc	acc	agt	gtg	agg	aca	cat	ttc	gcc	agg	ccg	aat	tgg	2956
Ile	Val	Ser	Gly	Thr	Ser	Val	Arg	Thr	His	Phe	Ala	Arg	Pro	Asn	Trp	
		925					930					935				
agg	aaa	gta	ttt	tcc	aag	acc	tta	acc	aag	cat	gca	aat	gca	aga	ata	3004
Arg	Lys	Val	Phe	Ser	Lys	Thr	Leu	Thr	Lys	His	Ala	Asn	Ala	Arg	Ile	
	940						945				950					
gga	gtt	ttc	tac	tgt	ggt	gca	ccc	ata	tta	gct	aaa	gaa	ctc	agc	caa	3052
Gly	Val	Phe	Tyr	Cys	Gly	Ala	Pro	Ile	Leu	Ala	Lys	Glu	Leu	Ser	Gln	
	955				960				965							
ctc	tcg	aaa	gag	ttt	aac	caa	aag	ggc	aca	aca	aag	ttc	gag	ttt	cac	3100
Leu	Cys	Lys	Glu	Phe	Asn	Gln	Lys	Gly	Thr	Thr	Lys	Phe	Glu	Phe	His	
	970				975				980					985		
aaa	gaa	cat	ttt	tagaagggcc	tggtgatga	ttaatcttgc	atcaacggta									3152
Lys	Glu	His	Phe													
cacacatcta	tcttcggtac	cttattttgat	tattctactg	aagagataaac	attagtaagg											3212
aataagtcag	agataaattg	tacataatag	ggaagaagac	tattttcaaga	gaaaatacat											3272
accaataaga	tgtgaaaaaaa	aaaaaaaaaaaa	aaaaactcgt	gccg												3316

&lt;210&gt; 10

&lt;211&gt; 989

&lt;212&gt; PRT

&lt;213&gt; Lycopersicon esculentum

&lt;400&gt; 10

Met	Arg	Gly	Leu	Pro	Gly	His	Glu	Arg	Arg	Trp	Thr	Ser	Asp	Thr	Val	
1				5					10					15		
Ser	Ser	Gly	Lys	Asp	Leu	Ser	Gly	Glu	Ser	Ser	Pro	Gly	Thr	Asp	Ser	
			20					25					30			
Gly	Asn	Ile	Ser	Gly	Phe	Ala	Ser	Glu	Glu	Phe	Val	Glu	Val	Ile	Leu	
		35					40					45				
Asp	Leu	Gln	Asp	Asp	Asp	Thr	Ile	Ile	Leu	Arg	Ser	Val	Glu	Pro	Ala	
	50					55				60						
Thr	Val	Ile	Asn	Ile	Asp	Gly	Ser	Asp	Pro	Ala	Ser	Gly	Val	Gly	Ile	
	65				70				75					80		
Gly	Gly	Ala	Ser	Ile	Glu	Thr	Pro	Ala	Ser	Val	Thr	Ser	Thr	Ser	Glu	
			85					90						95		
Thr	Arg	Ser	Pro	Met	Met	Arg	Arg	Ser	Thr	Ser	Asn	Lys	Phe	Arg	Gln	
			100					105					110			
Phe	Ser	Gln	Glu	Leu	Lys	Ala	Glu	Ala	Val	Ala	Lys	Ala	Lys	His	Phe	
		115					120				125					
Ser	Gln	Glu	Leu	Lys	Ala	Glu	Leu	Arg	Arg	Phe	Ser	Trp	Ser	His	Gly	
	130					135				140						
His	Ala	Ser	Arg	Ala	Phe	Ser	Pro	Ala	Ser	Phe	Gln	Asn	Ala	Val		
	145				150				155					160		

Val	Gly	Thr	Gly	Asn	Gly	Val	Asp	Ser	Ala	Leu	Ala	Ala	Arg	Ala	Leu	
				165					170					175		
Arg	Arg	Gln	Arg	Ala	Gln	Leu	Asp	Arg	Thr	Arg	Ser	Ser	Ala	His	Lys	
			180					185					190			
Ala	Leu	Arg	Gly	Leu	Lys	Phe	Ile	Ser	Asn	Asn	Lys	Thr	Asn	Gly	Trp	
		195					200					205				
Asn	Glu	Val	Glu	Asn	Asn	Phe	Ala	Lys	Leu	Ala	Lys	Asp	Gly	Tyr	Leu	
	210					215					220					
Tyr	Arg	Ser	Asp	Phe	Ala	Gln	Cys	Ile	Gly	Gln	Tyr	Ser	Arg	Arg	Arg	
225				230						235					240	
Ser	Leu	Gln	Phe	Asn	Tyr	Arg	Leu	Ile	Thr	Leu	Ile	Leu	Ile	Asn	Tyr	
			245						250					255		
Leu	Val	Lys	Gly	Met	Lys	Asp	Ser	Lys	Glu	Phe	Ala	Leu	Glu	Leu	Phe	
			260					265					270			
Asp	Ala	Leu	Ser	Arg	Arg	Arg	Arg	Leu	Lys	Val	Asp	Lys	Ile	Ser	Gln	
		275					280					285				
Glu	Glu	Leu	Tyr	Glu	Tyr	Trp	Ser	Gln	Ile	Thr	Asp	Gln	Ser	Phe	Asp	
	290					295					300					
Ser	Arg	Leu	Gln	Ile	Phe	Phe	Asp	Met	Val	Asp	Lys	Asn	Glu	Asp	Gly	
305				310						315					320	
Arg	Ile	Gly	Glu	Glu	Glu	Val	Lys	Glu	Ile	Ile	Met	Leu	Ser	Ala	Ser	
			325						330					335		
Ala	Asn	Lys	Leu	Ser	Arg	Leu	Lys	Glu	Gln	Ala	Glu	Glu	Tyr	Ala	Ala	
			340					345					350			
Leu	Ile	Met	Glu	Glu	Leu	Asp	Pro	Glu	Arg	Leu	Gly	Tyr	Ile	Glu	Leu	
		355					360					365				
Trp	Gln	Leu	Glu	Thr	Leu	Leu	Leu	Gln	Lys	Asp	Thr	Tyr	Leu	Asn	Tyr	
	370					375					380					
Ser	Gln	Ala	Leu	Ser	Tyr	Thr	Ser	Gln	Ala	Leu	Ser	Gln	Asn	Leu	Gln	
385					390					395					400	
Gly	Leu	Arg	Lys	Arg	Ser	Pro	Ile	Arg	Arg	Met	Ser	Thr	Lys	Leu	Val	
			405						410					415		
Tyr	Ser	Leu	Gln	Glu	Asn	Trp	Lys	Arg	Ile	Trp	Val	Leu	Val	Leu	Trp	
			420					425					430			
Ile	Leu	Ile	Met	Ile	Gly	Leu	Phe	Leu	Trp	Lys	Phe	Tyr	Gln	Tyr	Lys	
		435					440					445				
Gln	Lys	Ser	Ala	Phe	Gln	Val	Met	Gly	Tyr	Cys	Leu	Leu	Thr	Ala	Lys	
	450					455					460					
Gly	Ala	Ala	Glu	Thr	Leu	Lys	Phe	Asn	Met	Ala	Leu	Ile	Leu	Leu	Pro	
465					470					475					480	
Val	Cys	Arg	Asn	Thr	Ile	Thr	Phe	Leu	Arg	Ser	Thr	Lys	Leu	Ser	Cys	
			485						490					495		
Phe	Val	Pro	Phe	Asp	Asp	Asn	Ile	Asn	Phe	His	Lys	Thr	Val	Ala	Ala	
			500					505					510			
Ala	Ile	Val	Thr	Gly	Ile	Ile	Leu	His	Ala	Gly	Asn	His	Leu	Val	Cys	
		515					520					525				
Asp	Phe	Pro	Lys	Leu	Ile	His	Ala	Asn	Ser	Thr	Asn	Tyr	Gln	Lys	Tyr	
	530					535					540					
Leu	Val	Asn	Asp	Phe	Gly	Pro	Ser	Gln	Pro	Gln	Tyr	Ile	Asp	Leu	Val	
545					550					555					560	
Lys	Gly	Val	Glu	Gly	Val	Thr	Gly	Ile	Val	Met	Val	Ile	Leu	Met	Ala	
			565						570					575		
Ile	Ala	Phe	Thr	Leu	Ala	Thr	Arg	Trp	Phe	Arg	Arg	Ser	Leu	Ile	Lys	
			580					585					590			
Leu	Pro	Lys	Pro	Phe	Asp	Arg	Leu	Thr	Gly	Phe	Asn	Ala	Phe	Trp	Tyr	
		595					600					605				
Ser	His	His	Leu	Leu	Ile	Ile	Val	Tyr	Ile	Val	Leu	Ile	Ile	His	Gly	
	610					615					620					
Thr	Phe	Leu	Tyr	Leu	Val	His	Asn	Trp	Tyr	Ser	Lys	Thr	Thr	Trp	Met	
625					630					635					640	
Tyr	Ile	Ala	Val	Pro	Val	Leu	Leu	Tyr	Ala	Gly	Glu	Arg	Thr	Leu	Arg	

				645				650					655				
Phe	Phe	Arg	Ser	Gly	Leu	Tyr	Ser	Val	Arg	Leu	Leu	Lys	Val	Ala	Ile		
			660					665					670				
Tyr	Pro	Gly	Asn	Val	Leu	Thr	Leu	Gln	Met	Ser	Lys	Pro	Pro	Gln	Phe		
		675					680					685					
Arg	Tyr	Lys	Ser	Gly	Gln	Tyr	Met	Phe	Val	Gln	Cys	Pro	Ala	Val	Ser		
	690					695					700						
Pro	Phe	Glu	Trp	His	Pro	Phe	Ser	Ile	Thr	Ser	Ala	Pro	Gly	Asp	Asp		
705				710						715					720		
Tyr	Leu	Ser	Ile	His	Ile	Arg	Gln	Leu	Gly	Asp	Trp	Thr	Gln	Glu	Leu		
				725					730					735			
Lys	Arg	Val	Phe	Ser	Glu	Ala	Cys	Glu	Gln	Pro	Glu	Ala	Gly	Lys	Ser		
			740					745					750				
Gly	Leu	Leu	Arg	Ala	Asp	Glu	Asn	Thr	Lys	Thr	Ser	Leu	Pro	Lys	Leu		
		755					760					765					
Leu	Ile	Asp	Gly	Pro	Tyr	Gly	Ala	Pro	Ala	Gln	Asp	Tyr	Arg	Lys	Tyr		
	770					775					780						
Asp	Val	Leu	Leu	Leu	Val	Gly	Leu	Gly	Ile	Gly	Ala	Thr	Pro	Phe	Ile		
785					790					795					800		
Ser	Ile	Leu	Lys	Asp	Leu	Leu	Lys	Asn	Ile	Val	Ala	Met	Glu	Glu	Gln		
				805					810					815			
Ala	Asp	Leu	Val	Ser	Asp	Phe	Ser	Gly	Asn	Ser	Asp	Met	Ser	Ala	Ala		
			820					825					830				
Thr	Ser	Glu	Gln	Pro	Ala	Leu	Asn	Lys	Ile	Ser	Pro	Lys	Lys	Arg	Lys		
		835					840					845					
Ser	Thr	Leu	Lys	Thr	Thr	Asn	Ala	Tyr	Phe	Tyr	Trp	Val	Thr	Arg	Glu		
	850					855					860						
Gln	Gly	Ser	Phe	Asp	Trp	Phe	Lys	Gly	Val	Met	Asn	Glu	Val	Ala	Glu		
865					870					875					880		
Leu	Asp	Gln	Arg	Gly	Val	Ile	Glu	Met	His	Asn	Tyr	Leu	Thr	Ser	Val		
				885					890					895			
Tyr	Glu	Glu	Gly	Asp	Ala	Arg	Ser	Ala	Leu	Ile	Thr	Met	Val	Gln	Ala		
			900					905					910				
Leu	Asn	His	Ala	Lys	Asn	Gly	Val	Asp	Ile	Val	Ser	Gly	Thr	Ser	Val		
	915						920					925					
Arg	Thr	His	Phe	Ala	Arg	Pro	Asn	Trp	Arg	Lys	Val	Phe	Ser	Lys	Thr		
	930					935					940						
Leu	Thr	Lys	His	Ala	Asn	Ala	Arg	Ile	Gly	Val	Phe	Tyr	Cys	Gly	Ala		
945					950					955					960		
Pro	Ile	Leu	Ala	Lys	Glu	Leu	Ser	Gln	Leu	Cys	Lys	Glu	Phe	Asn	Gln		
				965					970					975			
Lys	Gly	Thr	Thr	Lys	Phe	Glu	Phe	His	Lys	Glu	His	Phe					
			980					985									

&lt;210&gt; 11

&lt;211&gt; 3080

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (15)..(2846)

&lt;223&gt; coding for NADPH oxidase

&lt;400&gt; 11

ccgacttttg	atct	atg	aaa	cgc	ttc	tca	aag	aac	gat	cgg	cga	cgg	tgg	50		
		Met	Lys	Pro	Phe	Ser	Lys	Asn	Asp	Arg	Arg	Arg	Trp			
		1				5					10					
tca	ttt	gat	tca	gtt	tcc	gcc	gga	aaa	acc	gcc	gtc	gga	agt	gca	tca	98
Ser	Phe	Asp	Ser	Val	Ser	Ala	Gly	Lys	Thr	Ala	Val	Gly	Ser	Ala	Ser	
		15				20					25					

act	tca	ccg	gga	act	gaa	tac	tcc	att	aac	ggg	gat	caa	gag	ttc	gtt	146
Thr	Ser	Pro	Gly	Thr	Glu	Tyr	Ser	Ile	Asn	Gly	Asp	Gln	Glu	Phe	Val	
	30					35					40					
gaa	gtc	aca	atc	gat	ctt	caa	gac	gat	gac	aca	atc	gtt	ctt	cgt	agc	194
Glu	Val	Thr	Ile	Asp	Leu	Gln	Asp	Asp	Asp	Thr	Ile	Val	Leu	Arg	Ser	
	45					50				55					60	
gtc	gag	cca	gca	acc	gcc	att	aat	gtc	atc	gga	gat	atc	tcc	gac	gac	242
Val	Glu	Pro	Ala	Thr	Ala	Ile	Asn	Val	Ile	Gly	Asp	Ile	Ser	Asp	Asp	
				65					70					75		
aac	acc	gga	ata	atg	act	ccg	gtt	tcg	att	tcg	aga	tct	ccg	acg	atg	290
Asn	Thr	Gly	Ile	Met	Thr	Pro	Val	Ser	Ile	Ser	Arg	Ser	Pro	Thr	Met	
			80					85					90			
aaa	cga	act	tca	tct	aat	cgg	ttc	cga	caa	ttc	tca	caa	gag	ctt	aaa	338
Lys	Arg	Thr	Ser	Ser	Asn	Arg	Phe	Arg	Gln	Phe	Ser	Gln	Glu	Leu	Lys	
		95					100					105				
gcc	gaa	gct	gtg	gcg	aaa	gcg	aaa	cag	tta	tct	cag	gag	ttg	aaa	cga	386
Ala	Glu	Ala	Val	Ala	Lys	Ala	Lys	Gln	Leu	Ser	Gln	Glu	Leu	Lys	Arg	
	110					115					120					
ttc	tca	tgg	tct	cgt	tct	ttc	tca	ggg	aac	tta	acc	act	act	agt	acc	434
Phe	Ser	Trp	Ser	Arg	Ser	Phe	Ser	Gly	Asn	Leu	Thr	Thr	Thr	Ser	Thr	
	125				130				135						140	
gcc	gct	aat	caa	agc	ggc	ggg	gct	ggg	ggg	ggg	ttg	gtg	aac	tcg	gct	482
Ala	Ala	Asn	Gln	Ser	Gly	Gly	Ala	Gly	Gly	Gly	Leu	Val	Asn	Ser	Ala	
				145				150					155			
tta	gaa	gcg	cga	gcg	ttg	cga	aag	caa	cgt	gct	cag	tta	gat	cgg	act	530
Leu	Glu	Ala	Arg	Ala	Leu	Arg	Lys	Gln	Arg	Ala	Gln	Leu	Asp	Arg	Thr	
			160					165					170			
cgg	tct	agt	gct	caa	aga	gct	ctt	cgt	ggg	ttg	aga	ttc	att	agc	aat	578
Arg	Ser	Ser	Ala	Gln	Arg	Ala	Leu	Arg	Gly	Leu	Arg	Phe	Ile	Ser	Asn	
			175				180					185				
aag	caa	aag	aac	gtt	gat	ggg	tgg	aac	gat	gtt	caa	tca	aat	ttc	gaa	626
Lys	Gln	Lys	Asn	Val	Asp	Gly	Trp	Asn	Asp	Val	Gln	Ser	Asn	Phe	Glu	
	190					195					200					
aaa	ttc	gaa	aaa	aat	ggg	tac	atc	tat	cgc	tcc	gat	ttc	gct	caa	tgc	674
Lys	Phe	Glu	Lys	Asn	Gly	Tyr	Ile	Tyr	Arg	Ser	Asp	Phe	Ala	Gln	Cys	
	205				210					215					220	
ata	gga	atg	aaa	gat	tcg	aaa	gaa	ttt	gca	ttg	gaa	ctg	ttc	gat	gca	722
Ile	Gly	Met	Lys	Asp	Ser	Lys	Glu	Phe	Ala	Leu	Glu	Leu	Phe	Asp	Ala	
				225					230					235		
ttg	agt	aga	aga	aga	aga	tta	aaa	gta	gag	aaa	atc	aat	cac	gat	gag	770
Leu	Ser	Arg	Arg	Arg	Arg	Leu	Lys	Val	Glu	Lys	Ile	Asn	His	Asp	Glu	
				240				245					250			
ctt	tat	gag	tat	tgg	tca	caa	atc	aac	gac	gag	agt	ttt	gat	tct	cgt	818
Leu	Tyr	Glu	Tyr	Trp	Ser	Gln	Ile	Asn	Asp	Glu	Ser	Phe	Asp	Ser	Arg	
		255				260						265				
ctc	cag	atc	ttc	ttc	gac	ata	gtg	gac	aag	aat	gaa	gat	ggg	aga	att	866
Leu	Gln	Ile	Phe	Phe	Asp	Ile	Val	Asp	Lys	Asn	Glu	Asp	Gly	Arg	Ile	
	270					275					280					
aca	gaa	gag	gaa	gta	aaa	gag	ata	ata	atg	ttg	agt	gca	tct	gca	aat	914
Thr	Glu	Glu	Glu	Val	Lys	Glu	Ile	Ile	Met	Leu	Ser	Ala	Ser	Ala	Asn	
	285				290					295					300	
aag	cta	tca	aga	tta	aag	gaa	caa	gca	gag	gaa	tat	gca	gct	ttg	att	962
Lys	Leu	Ser	Arg	Leu	Lys	Glu	Gln	Ala	Glu	Glu	Tyr	Ala	Ala	Leu	Ile	
				305					310					315		
atg	gaa	gag	tta	gat	cct	gaa	aga	ctt	ggc	tac	ata	gag	cta	tgg	caa	1010
Met	Glu	Glu	Leu	Asp	Pro	Glu	Arg	Leu	Gly	Tyr	Ile	Glu	Leu	Trp	Gln	
			320					325					330			
cta	gag	act	ttg	ctt	cta	caa	aaa	gac	aca	tac	ctc	aat	tac	agt	caa	1058
Leu	Glu	Thr	Leu	Leu	Leu	Gln	Lys	Asp	Thr	Tyr	Leu	Asn	Tyr	Ser	Gln	
		335				340						345				
gca	ttg	agc	tat	acg	agc	caa	gca	ttg	agc	caa	aac	ctt	caa	ggg	tta	1106

Ala	Leu	Ser	Tyr	Thr	Ser	Gln	Ala	Leu	Ser	Gln	Asn	Leu	Gln	Gly	Leu	
350						355					360					
agg	gga	aag	agt	cga	ata	cat	aga	atg	agt	tcg	gat	ttc	gtc	tac	att	1154
Arg	Gly	Lys	Ser	Arg	Ile	His	Arg	Met	Ser	Ser	Asp	Phe	Val	Tyr	Ile	
365						370					375				380	
atg	caa	gag	aat	tgg	aaa	agg	ata	tgg	gtt	tta	tcc	tta	tgg	atc	atg	1202
Met	Gln	Glu	Asn	Trp	Lys	Arg	Ile	Trp	Val	Leu	Ser	Leu	Trp	Ile	Met	
				385					390					395		
atc	atg	atc	gga	tta	ttc	ttg	tgg	aaa	ttc	ttc	caa	tac	aag	caa	aaa	1250
Ile	Met	Ile	Gly	Leu	Phe	Leu	Trp	Lys	Phe	Phe	Gln	Tyr	Lys	Gln	Lys	
			400					405				410				
gat	gca	ttt	cat	gtg	atg	gga	tat	tgt	tta	ctc	aca	gcc	aaa	gga	gca	1298
Asp	Ala	Phe	His	Val	Met	Gly	Tyr	Cys	Leu	Leu	Thr	Ala	Lys	Gly	Ala	
		415				420					425					
gct	gaa	aca	ctt	aaa	ttc	aac	atg	gct	cta	ata	ctt	ttc	cca	gtt	tgc	1346
Ala	Glu	Thr	Leu	Lys	Phe	Asn	Met	Ala	Leu	Ile	Leu	Phe	Pro	Val	Cys	
	430					435					440					
aga	aac	acc	att	act	tgg	ctt	aga	tcc	aca	aga	ctc	tct	tac	ttc	gtt	1394
Arg	Asn	Thr	Ile	Thr	Trp	Leu	Arg	Ser	Thr	Arg	Leu	Ser	Tyr	Phe	Val	
	445				450					455					460	
cct	ttt	gat	gat	aat	atc	aac	ttc	cac	aag	aca	att	gct	gga	gcc	att	1442
Pro	Phe	Asp	Asp	Asn	Ile	Asn	Phe	His	Lys	Thr	Ile	Ala	Gly	Ala	Ile	
				465					470				475			
gta	gta	gct	gtg	atc	ctt	cat	att	gga	gac	cat	ctt	gct	tgt	gat	ttc	1490
Val	Val	Ala	Val	Ile	Leu	His	Ile	Gly	Asp	His	Leu	Ala	Cys	Asp	Phe	
			480					485				490				
cct	aga	att	gtt	aga	gcc	acc	gaa	tac	gat	tac	aat	cgg	tat	ctg	ttt	1538
Pro	Arg	Ile	Val	Arg	Ala	Thr	Glu	Tyr	Asp	Tyr	Asn	Arg	Tyr	Leu	Phe	
	495					500					505					
cat	tac	ttt	caa	aca	aaa	cag	cca	aca	tac	ttc	gac	ctc	gtt	aag	gga	1586
His	Tyr	Phe	Gln	Thr	Lys	Gln	Pro	Thr	Tyr	Phe	Asp	Leu	Val	Lys	Gly	
	510					515					520					
cct	gaa	gga	atc	act	ggg	att	tta	atg	gtc	att	ttg	atg	att	att	tca	1634
Pro	Glu	Gly	Ile	Thr	Gly	Ile	Leu	Met	Val	Ile	Leu	Met	Ile	Ile	Ser	
	525				530					535					540	
ttc	aca	tta	gca	aca	aga	tgg	ttt	agg	cgt	aac	cta	gtc	aag	ctt	cct	1682
Phe	Thr	Leu	Ala	Thr	Arg	Trp	Phe	Arg	Arg	Asn	Leu	Val	Lys	Leu	Pro	
			545						550					555		
aag	cca	ttt	gat	cga	cta	acc	ggg	ttt	aac	gcc	ttt	tgg	tat	tcg	cat	1730
Lys	Pro	Phe	Asp	Arg	Leu	Thr	Gly	Phe	Asn	Ala	Phe	Trp	Tyr	Ser	His	
			560				565						570			
cat	ttg	ttc	gtc	att	gtt	tat	atc	ttg	ctt	att	ctt	cat	ggg	atc	ttc	1778
His	Leu	Phe	Val	Ile	Val	Tyr	Ile	Leu	Leu	Ile	Leu	His	Gly	Ile	Phe	
		575				580					585					
ctc	tat	ttc	gcc	aag	cct	tgg	tat	gtt	cgt	acg	aca	tgg	atg	tat	ctt	1826
Leu	Tyr	Phe	Ala	Lys	Pro	Trp	Tyr	Val	Arg	Thr	Thr	Trp	Met	Tyr	Leu	
	590					595					600					
gca	gta	cca	gtt	tta	ctc	tat	ggg	gga	gaa	aga	aca	ctt	agg	tac	ttc	1874
Ala	Val	Pro	Val	Leu	Leu	Tyr	Gly	Gly	Glu	Arg	Thr	Leu	Arg	Tyr	Phe	
	605				610				615						620	
cgt	tct	ggg	tct	tat	tcg	gtt	cga	ctg	ctt	aag	gtt	gct	ata	tat	cct	1922
Arg	Ser	Gly	Ser	Tyr	Ser	Val	Arg	Leu	Leu	Lys	Val	Ala	Ile	Tyr	Pro	
			625						630					635		
ggg	aat	gtt	cta	acg	cta	caa	atg	tcg	aaa	cca	act	caa	ttt	cgt	tac	1970
Gly	Asn	Val	Leu	Thr	Leu	Gln	Met	Ser	Lys	Pro	Thr	Gln	Phe	Arg	Tyr	
			640					645					650			
aaa	agc	gga	caa	tac	atg	ttt	gtc	caa	tgt	cct	gcg	gtt	tcg	cca	ttc	2018
Lys	Ser	Gly	Gln	Tyr	Met	Phe	Val	Gln	Cys	Pro	Ala	Val	Ser	Pro	Phe	
		655				660						665				
gag	tgg	cat	cca	ttc	tca	att	act	tcc	gca	cct	gaa	gat	gat	tat	atc	2066
Glu	Trp	His	Pro	Phe	Ser	Ile	Thr	Ser	Ala	Pro	Glu	Asp	Asp	Tyr	Ile	



```

        670                675                680
agc att cac att aga caa ctt ggt gat tgg act caa gaa ctc aaa aga 2114
Ser Ile His Ile Arg Gln Leu Gly Asp Trp Thr Gln Glu Leu Lys Arg
685                690                695                700
gta ttc tct gaa gtt tgt gag cca ccg gtt ggc ggt aaa agc gga ctt 2162
Val Phe Ser Glu Val Cys Glu Pro Pro Val Gly Gly Lys Ser Gly Leu
        705                710                715
ctc aga gcc gac gaa aca aca aag aaa agt ttg cca aag cta ttg ata 2210
Leu Arg Ala Asp Glu Thr Thr Lys Lys Ser Leu Pro Lys Leu Leu Ile
        720                725                730
gat gga ccg tac ggt gca cca gca caa gat tat agg aaa tat gat gtt 2258
Asp Gly Pro Tyr Gly Ala Pro Ala Gln Asp Tyr Arg Lys Tyr Asp Val
        735                740                745
ctc tta tta gtt ggt ctt ggc att ggt gca act cca ttt atc agt atc 2306
Leu Leu Leu Val Gly Leu Gly Ile Gly Ala Thr Pro Phe Ile Ser Ile
        750                755                760
ttg aaa gat ttg ctt aac aac att gtt aaa atg gaa gag cat gcg gat 2354
Leu Lys Asp Leu Leu Asn Asn Ile Val Lys Met Glu Glu His Ala Asp
        765                770                775                780
tcg atc tcg gat ttc agt aga tca tca gaa tac agc aca gga agc aac 2402
Ser Ile Ser Asp Phe Ser Arg Ser Ser Glu Tyr Ser Thr Gly Ser Asn
        785                790                795
ggt gac acg cca aga cga aag aga ata cta aaa acc aca aat gct tat 2450
Gly Asp Thr Pro Arg Arg Lys Arg Ile Leu Lys Thr Thr Asn Ala Tyr
        800                805                810
ttc tac tgg gtc aca aga gaa caa ggc tct ttt gat tgg ttc aaa ggt 2498
Phe Tyr Trp Val Thr Arg Glu Gln Gly Ser Phe Asp Trp Phe Lys Gly
        815                820                825
gtc atg aac gaa gtt gca gaa ctt gac caa cgg ggt gtg ata gag atg 2546
Val Met Asn Glu Val Ala Glu Leu Asp Gln Arg Gly Val Ile Glu Met
        830                835                840
cat aac tat tta aca agt gtg tat gaa gaa ggt gat gct cgt tct gct 2594
His Asn Tyr Leu Thr Ser Val Tyr Glu Glu Gly Asp Ala Arg Ser Ala
        845                850                855                860
ctc att aca atg gtt caa gct ctt aat cat gcc aaa aat ggt gtc gac 2642
Leu Ile Thr Met Val Gln Ala Leu Asn His Ala Lys Asn Gly Val Asp
        865                870                875
att gtc tct ggc act agg gtc aga aca cac ttt gca aga cct aat tgg 2690
Ile Val Ser Gly Thr Arg Val Arg Thr His Phe Ala Arg Pro Asn Trp
        880                885                890
aag aag gtt ctc aca aag cta agt tcc aag cat tgc aat gca aga aca 2738
Lys Lys Val Leu Thr Lys Leu Ser Ser Lys His Cys Asn Ala Arg Thr
        895                900                905
gga gtg ttt tat tgc gga gta ccg gtt tta ggg aag gag ctt agc aaa 2786
Gly Val Phe Tyr Cys Gly Val Pro Val Leu Gly Lys Glu Leu Ser Lys
        910                915                920
cta tgc aac aca ttc aat caa aaa ggt tca acc aag ttt gaa ttt cac 2834
Leu Cys Asn Thr Phe Asn Gln Lys Gly Ser Thr Lys Phe Glu Phe His
        925                930                935                940
aag gag cat ttc taaaagacaa gaaggaagaa gccaaaagcc ctctagattc 2886
Lys Glu His Phe
ttaaataatct caaatttagc cacttatagt ataaaggcaa tctcttcact atttaattca 2946
aagtgattaa acgttaacac actgtcaaaa gtgagtgtgt taacgttttag ctccacacgt 3006
tctaggttta tatacaccga ggcatacgtg taaatatacg agacagaaga aattcaaggg 3066
ggtttgatag aagc 3080

```

&lt;210&gt; 12

&lt;211&gt; 944

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 12

Met	Lys	Pro	Phe	Ser	Lys	Asn	Asp	Arg	Arg	Arg	Trp	Ser	Phe	Asp	Ser
1				5					10					15	
Val	Ser	Ala	Gly	Lys	Thr	Ala	Val	Gly	Ser	Ala	Ser	Thr	Ser	Pro	Gly
			20					25					30		
Thr	Glu	Tyr	Ser	Ile	Asn	Gly	Asp	Gln	Glu	Phe	Val	Glu	Val	Thr	Ile
		35					40					45			
Asp	Leu	Gln	Asp	Asp	Asp	Thr	Ile	Val	Leu	Arg	Ser	Val	Glu	Pro	Ala
	50					55					60				
Thr	Ala	Ile	Asn	Val	Ile	Gly	Asp	Ile	Ser	Asp	Asp	Asn	Thr	Gly	Ile
	65				70					75					80
Met	Thr	Pro	Val	Ser	Ile	Ser	Arg	Ser	Pro	Thr	Met	Lys	Arg	Thr	Ser
				85					90					95	
Ser	Asn	Arg	Phe	Arg	Gln	Phe	Ser	Gln	Glu	Leu	Lys	Ala	Glu	Ala	Val
			100					105					110		
Ala	Lys	Ala	Lys	Gln	Leu	Ser	Gln	Glu	Leu	Lys	Arg	Phe	Ser	Trp	Ser
		115					120					125			
Arg	Ser	Phe	Ser	Gly	Asn	Leu	Thr	Thr	Thr	Ser	Thr	Ala	Ala	Asn	Gln
	130					135					140				
Ser	Gly	Gly	Ala	Gly	Gly	Gly	Leu	Val	Asn	Ser	Ala	Leu	Glu	Ala	Arg
	145				150					155					160
Ala	Leu	Arg	Lys	Gln	Arg	Ala	Gln	Leu	Asp	Arg	Thr	Arg	Ser	Ser	Ala
			165						170					175	
Gln	Arg	Ala	Leu	Arg	Gly	Leu	Arg	Phe	Ile	Ser	Asn	Lys	Gln	Lys	Asn
			180					185					190		
Val	Asp	Gly	Trp	Asn	Asp	Val	Gln	Ser	Asn	Phe	Glu	Lys	Phe	Glu	Lys
		195					200					205			
Asn	Gly	Tyr	Ile	Tyr	Arg	Ser	Asp	Phe	Ala	Gln	Cys	Ile	Gly	Met	Lys
	210					215					220				
Asp	Ser	Lys	Glu	Phe	Ala	Leu	Glu	Leu	Phe	Asp	Ala	Leu	Ser	Arg	Arg
	225				230					235					240
Arg	Arg	Leu	Lys	Val	Glu	Lys	Ile	Asn	His	Asp	Glu	Leu	Tyr	Glu	Tyr
			245						250					255	
Trp	Ser	Gln	Ile	Asn	Asp	Glu	Ser	Phe	Asp	Ser	Arg	Leu	Gln	Ile	Phe
			260					265					270		
Phe	Asp	Ile	Val	Asp	Lys	Asn	Glu	Asp	Gly	Arg	Ile	Thr	Glu	Glu	Glu
		275					280					285			
Val	Lys	Glu	Ile	Ile	Met	Leu	Ser	Ala	Ser	Ala	Asn	Lys	Leu	Ser	Arg
	290					295					300				
Leu	Lys	Glu	Gln	Ala	Glu	Glu	Tyr	Ala	Ala	Leu	Ile	Met	Glu	Glu	Leu
	305				310					315					320
Asp	Pro	Glu	Arg	Leu	Gly	Tyr	Ile	Glu	Leu	Trp	Gln	Leu	Glu	Thr	Leu
			325						330					335	
Leu	Leu	Gln	Lys	Asp	Thr	Tyr	Leu	Asn	Tyr	Ser	Gln	Ala	Leu	Ser	Tyr
			340					345					350		
Thr	Ser	Gln	Ala	Leu	Ser	Gln	Asn	Leu	Gln	Gly	Leu	Arg	Gly	Lys	Ser
		355					360					365			
Arg	Ile	His	Arg	Met	Ser	Ser	Asp	Phe	Val	Tyr	Ile	Met	Gln	Glu	Asn
	370					375					380				
Trp	Lys	Arg	Ile	Trp	Val	Leu	Ser	Leu	Trp	Ile	Met	Ile	Met	Ile	Gly
	385				390					395					400
Leu	Phe	Leu	Trp	Lys	Phe	Phe	Gln	Tyr	Lys	Gln	Lys	Asp	Ala	Phe	His
			405						410					415	
Val	Met	Gly	Tyr	Cys	Leu	Leu	Thr	Ala	Lys	Gly	Ala	Ala	Glu	Thr	Leu
			420					425					430		
Lys	Phe	Asn	Met	Ala	Leu	Ile	Leu	Phe	Pro	Val	Cys	Arg	Asn	Thr	Ile
		435					440					445			
Thr	Trp	Leu	Arg	Ser	Thr	Arg	Leu	Ser	Tyr	Phe	Val	Pro	Phe	Asp	Asp
	450					455					460				
Asn	Ile	Asn	Phe	His	Lys	Thr	Ile	Ala	Gly	Ala	Ile	Val	Val	Ala	Val
	465				470					475					480

Ile	Leu	His	Ile	Gly	Asp	His	Leu	Ala	Cys	Asp	Phe	Pro	Arg	Ile	Val
				485					490					495	
Arg	Ala	Thr	Glu	Tyr	Asp	Tyr	Asn	Arg	Tyr	Leu	Phe	His	Tyr	Phe	Gln
			500					505					510		
Thr	Lys	Gln	Pro	Thr	Tyr	Phe	Asp	Leu	Val	Lys	Gly	Pro	Glu	Gly	Ile
		515					520					525			
Thr	Gly	Ile	Leu	Met	Val	Ile	Leu	Met	Ile	Ile	Ser	Phe	Thr	Leu	Ala
	530					535					540				
Thr	Arg	Trp	Phe	Arg	Arg	Asn	Leu	Val	Lys	Leu	Pro	Lys	Pro	Phe	Asp
545					550					555					560
Arg	Leu	Thr	Gly	Phe	Asn	Ala	Phe	Trp	Tyr	Ser	His	His	Leu	Phe	Val
			565						570					575	
Ile	Val	Tyr	Ile	Leu	Leu	Ile	Leu	His	Gly	Ile	Phe	Leu	Tyr	Phe	Ala
			580					585					590		
Lys	Pro	Trp	Tyr	Val	Arg	Thr	Thr	Trp	Met	Tyr	Leu	Ala	Val	Pro	Val
		595					600					605			
Leu	Leu	Tyr	Gly	Gly	Glu	Arg	Thr	Leu	Arg	Tyr	Phe	Arg	Ser	Gly	Ser
	610					615					620				
Tyr	Ser	Val	Arg	Leu	Leu	Lys	Val	Ala	Ile	Tyr	Pro	Gly	Asn	Val	Leu
625					630					635					640
Thr	Leu	Gln	Met	Ser	Lys	Pro	Thr	Gln	Phe	Arg	Tyr	Lys	Ser	Gly	Gln
			645						650					655	
Tyr	Met	Phe	Val	Gln	Cys	Pro	Ala	Val	Ser	Pro	Phe	Glu	Trp	His	Pro
			660					665					670		
Phe	Ser	Ile	Thr	Ser	Ala	Pro	Glu	Asp	Asp	Tyr	Ile	Ser	Ile	His	Ile
		675					680					685			
Arg	Gln	Leu	Gly	Asp	Trp	Thr	Gln	Glu	Leu	Lys	Arg	Val	Phe	Ser	Glu
	690					695					700				
Val	Cys	Glu	Pro	Pro	Val	Gly	Gly	Lys	Ser	Gly	Leu	Leu	Arg	Ala	Asp
705					710					715					720
Glu	Thr	Thr	Lys	Lys	Ser	Leu	Pro	Lys	Leu	Leu	Ile	Asp	Gly	Pro	Tyr
			725						730					735	
Gly	Ala	Pro	Ala	Gln	Asp	Tyr	Arg	Lys	Tyr	Asp	Val	Leu	Leu	Leu	Val
			740					745					750		
Gly	Leu	Gly	Ile	Gly	Ala	Thr	Pro	Phe	Ile	Ser	Ile	Leu	Lys	Asp	Leu
		755					760					765			
Leu	Asn	Asn	Ile	Val	Lys	Met	Glu	Glu	His	Ala	Asp	Ser	Ile	Ser	Asp
	770					775						780			
Phe	Ser	Arg	Ser	Ser	Glu	Tyr	Ser	Thr	Gly	Ser	Asn	Gly	Asp	Thr	Pro
785					790					795					800
Arg	Arg	Lys	Arg	Ile	Leu	Lys	Thr	Thr	Asn	Ala	Tyr	Phe	Tyr	Trp	Val
			805						810					815	
Thr	Arg	Glu	Gln	Gly	Ser	Phe	Asp	Trp	Phe	Lys	Gly	Val	Met	Asn	Glu
		820						825					830		
Val	Ala	Glu	Leu	As											

<210> 13  
<211> 3035

&lt;212&gt; DNA

<213> *Arabidopsis thaliana*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (132)..(2894)

&lt;223&gt; coding for NADPH oxidase

&lt;400&gt; 13

```

tcaaacacct tttgagagcg gttatTTTTT ctctatcaac taatacagta accttacggg 60
tggtttatttg tatagatctc tgtggTTTTT ttggccaact ctagtgagat ctttttcggt 120
tctcgaattc g atg aaa atg aga cga ggc aat tca agt aac gac cat gaa 170
          Met Lys Met Arg Arg Gly Asn Ser Ser Asn Asp His Glu
                1             5             10
ctt ggg att cta cga gga gct aac tcg gac acc aac tcg gac acg gag 218
Leu Gly Ile Leu Arg Gly Ala Asn Ser Asp Thr Asn Ser Asp Thr Glu
          15             20             25
agc atc gct agc gac cgt ggt gcc ttt agc ggt ccg ctt ggc cgg cct 266
Ser Ile Ala Ser Asp Arg Gly Ala Phe Ser Gly Pro Leu Gly Arg Pro
          30             35             40             45
aaa cgt gcg tcc aag aaa aac gca aga ttc gcc gac gat ctt ccc aag 314
Lys Arg Ala Ser Lys Lys Asn Ala Arg Phe Ala Asp Asp Leu Pro Lys
                50             55             60
aga agc aat agt gtt gct ggc ggc cgt ggt gat gac gat gag tac gtg 362
Arg Ser Asn Ser Val Ala Gly Gly Arg Gly Asp Asp Asp Glu Tyr Val
                65             70             75
gag atc acg cta gac atc agg gac gac tcg gtg gcc gtc cat agt gtc 410
Glu Ile Thr Leu Asp Ile Arg Asp Asp Ser Val Ala Val His Ser Val
                80             85             90
caa caa gca gct gga ggt gga ggc cac ctg gag gac ccg gag cta gcc 458
Gln Gln Ala Ala Gly Gly Gly Gly His Leu Glu Asp Pro Glu Leu Ala
          95             100             105
ctt ctt acg aag aag act ctc gag agc agc ctc aac aac acc acc tcc 506
Leu Leu Thr Lys Lys Thr Leu Glu Ser Ser Leu Asn Asn Thr Thr Ser
          110             115             120
tta tct ttc ttc cga agc acc tcc tca cgc atc aag aac gcc tcc cgc 554
Leu Ser Phe Phe Arg Ser Thr Ser Ser Arg Ile Lys Asn Ala Ser Arg
                130             135             140
gag ctc cgc cgc gtg ttc tct aga cgt ccc tcc ccg gcc gtg cgg cgg 602
Glu Leu Arg Arg Val Phe Ser Arg Arg Pro Ser Pro Ala Val Arg Arg
                145             150             155
ttt gac cgc acg agc tcc gcg gcc atc cac gca ctc aaa ggt ctc aag 650
Phe Asp Arg Thr Ser Ser Ala Ala Ile His Ala Leu Lys Gly Leu Lys
          160             165             170
ttc att gcc acc aag acg gcc gca tgg ccg gcc gtc gac caa cgt ttc 698
Phe Ile Ala Thr Lys Thr Ala Ala Trp Pro Ala Val Asp Gln Arg Phe
          175             180             185
gat aaa ctc tcc gct gat tcc aac ggc ctc tta ctc tct gcc aag ttt 746
Asp Lys Leu Ser Ala Asp Ser Asn Gly Leu Leu Leu Ser Ala Lys Phe
          190             195             200
tgg gaa tgc tta gga atg aat aag gaa tct aaa gac ttc gct gac cag 794
Trp Glu Cys Leu Gly Met Asn Lys Glu Ser Lys Asp Phe Ala Asp Gln
                210             215             220
ctc ttt aga gca tta gct cgc cgg aat aac gtc tcc ggc gat gca atc 842
Leu Phe Arg Ala Leu Ala Arg Arg Asn Asn Val Ser Gly Asp Ala Ile
                225             230             235
aca aag gaa cag ctt agg ata ttc tgg gaa cag atc tca gac gaa agc 890
Thr Lys Glu Gln Leu Arg Ile Phe Trp Glu Gln Ile Ser Asp Glu Ser
          240             245             250
ttt gat gcc aaa ctc caa gtc ttt ttt gac atg gtg gac aaa gat gaa 938
Phe Asp Ala Lys Leu Gln Val Phe Phe Asp Met Val Asp Lys Asp Glu

```

	255					260					265					
gat	ggg	cga	gta	aca	gaa	gaa	gag	gtg	gct	gag	att	att	agt	ctt	agt	986
Asp	Gly	Arg	Val	Thr	Glu	Glu	Glu	Val	Ala	Glu	Ile	Ile	Ser	Leu	Ser	
270					275					280					285	
gct	tct	gca	aac	aag	ctc	tca	aat	att	caa	aag	caa	gcc	aaa	gaa	tat	1034
Ala	Ser	Ala	Asn	Lys	Leu	Ser	Asn	Ile	Gln	Lys	Gln	Ala	Lys	Glu	Tyr	
				290					295					300		
gcg	gca	ctg	ata	atg	gaa	gag	ttg	gac	cca	gac	aat	gct	ggg	ttt	att	1082
Ala	Ala	Leu	Ile	Met	Glu	Glu	Leu	Asp	Pro	Asp	Asn	Ala	Gly	Phe	Ile	
			305					310					315			
atg	atc	gaa	aac	ttg	gaa	atg	ttg	cta	tta	caa	gca	ccg	aac	cag	tcg	1130
Met	Ile	Glu	Asn	Leu	Glu	Met	Leu	Leu	Leu	Gln	Ala	Pro	Asn	Gln	Ser	
			320				325					330				
gtg	cgg	atg	gga	gac	agc	agg	ata	ctt	agt	cag	atg	tta	agt	cag	aag	1178
Val	Arg	Met	Gly	Asp	Ser	Arg	Ile	Leu	Ser	Gln	Met	Leu	Ser	Gln	Lys	
			335			340					345					
ctt	aga	ccg	gca	aaa	gag	agc	aac	cct	tta	ttg	aga	tggt	tcg	gag	aaa	1226
Leu	Arg	Pro	Ala	Lys	Glu	Ser	Asn	Pro	Leu	Leu	Arg	Trp	Ser	Glu	Lys	
350					355					360					365	
atc	aaa	tat	ttc	ata	ctt	gat	aat	tgg	cag	aga	tta	tgg	atc	atg	atg	1274
Ile	Lys	Tyr	Phe	Ile	Leu	Asp	Asn	Trp	Gln	Arg	Leu	Trp	Ile	Met	Met	
			370						375					380		
tta	tgg	ctt	ggc	atc	tgt	ggg	ggc	ctc	ttt	act	tat	aaa	ttc	att	cag	1322
Leu	Trp	Leu	Gly	Ile	Cys	Gly	Gly	Leu	Phe	Thr	Tyr	Lys	Phe	Ile	Gln	
			385				390						395			
tac	aag	aac	aaa	gct	gcc	tat	ggg	gtg	atg	ggg	tat	tgt	ggt	tgt	gtc	1370
Tyr	Lys	Asn	Lys	Ala	Ala	Tyr	Gly	Val	Met	Gly	Tyr	Cys	Val	Cys	Val	
			400				405					410				
gcc	aaa	gga	ggc	gcc	gag	act	ctc	aaa	ttc	aac	atg	gct	ctc	ata	ttg	1418
Ala	Lys	Gly	Gly	Ala	Glu	Thr	Leu	Lys	Phe	Asn	Met	Ala	Leu	Ile	Leu	
			415			420					425					
ttg	cct	ggt	tgt	cga	aac	acc	atc	act	tgg	ctt	agg	aac	aag	acc	aag	1466
Leu	Pro	Val	Cys	Arg	Asn	Thr	Ile	Thr	Trp	Leu	Arg	Asn	Lys	Thr	Lys	
430					435					440				445		
ctt	ggg	act	gtc	ggt	cct	ttt	gat	gat	agt	ctt	aac	ttc	cac	aag	ggt	1514
Leu	Gly	Thr	Val	Val	Pro	Phe	Asp	Asp	Ser	Leu	Asn	Phe	His	Lys	Val	
			450						455					460		
att	gca	agc	ggg	ata	gtc	gtc	ggg	ggt	ttg	ctc	cat	gcg	ggg	gcc	cat	1562
Ile	Ala	Ser	Gly	Ile	Val	Val	Gly	Val	Leu	Leu	His	Ala	Gly	Ala	His	
			465				470						475			
tta	acg	tgt	gat	ttt	cca	cgt	tta	att	gcc	gcg	gat	gag	gac	acc	tat	1610
Leu	Thr	Cys	Asp	Phe	Pro	Arg	Leu	Ile	Ala	Ala	Asp	Glu	Asp	Thr	Tyr	
			480				485					490				
gag	ccg	atg	gaa	aaa	tac	ttt	ggg	gat	caa	ccg	act	agc	tac	tgg	tgg	1658
Glu	Pro	Met	Glu	Lys	Tyr	Phe	Gly	Asp	Gln	Pro	Thr	Ser	Tyr	Trp	Trp	
			495			500					505					
ttt	gtg	aaa	gga	gtg	gaa	gga	tgg	act	ggc	att	gtg	atg	ggt	gtg	cta	1706
Phe	Val	Lys	Gly	Val	Glu	Gly	Trp	Thr	Gly	Ile	Val	Met	Val	Val	Leu	
510					515					520					525	
atg	gct	ata	gcc	ttt	aca	ctc	gct	acg	cct	tgg	ttc	cga	cgt	aac	aag	1754
Met	Ala	Ile	Ala	Phe	Thr	Leu	Ala	Thr	Pro	Trp	Phe	Arg	Arg	Asn	Lys	
				530					535					540		
ctt	aac	tta	cct	aac	ttc	ctc	aag	aag	ctt	acc	ggg	ttc	aac	gcc	ttt	1802
Leu	Asn	Leu	Pro	Asn	Phe	Leu	Lys	Lys	Leu	Thr	Gly	Phe	Asn	Ala	Phe	
			545					550					555			
tgg	tac	acc	cac	cat	ttg	ttc	atc	att	gtt	tat	gct	ctt	ctc	att	gtc	1850
Trp	Tyr	Thr	His	His	Leu	Phe	Ile	Ile	Val	Tyr	Ala	Leu	Leu	Ile	Val	
			560			565						570				
cat	ggg	atc	aag	ctc	tac	ctc	aca	aag	att	tgg	tat	cag	aag	acg	aca	1898
His	Gly	Ile	Lys	Leu	Tyr	Leu	Thr	Lys	Ile	Trp	Tyr	Gln	Lys	Thr	Thr	
			575			580					585					

tgg	atg	tat	ctt	gct	gta	ccc	atc	ctt	cta	tat	gca	tct	gag	agg	ctg	1946
Trp	Met	Tyr	Leu	Ala	Val	Pro	Ile	Leu	Leu	Tyr	Ala	Ser	Glu	Arg	Leu	
590					595				600						605	
ctc	cgt	gct	ttc	aga	tca	agc	atc	aaa	ccg	gtt	aag	atg	atc	aag	gtg	1994
Leu	Arg	Ala	Phe	Arg	Ser	Ser	Ile	Lys	Pro	Val	Lys	Met	Ile	Lys	Val	
				610					615						620	
gct	gtt	tac	ccc	ggg	aac	gtg	ttg	tct	cta	cac	atg	acg	aag	cca	caa	2042
Ala	Val	Tyr	Pro	Gly	Asn	Val	Leu	Ser	Leu	His	Met	Thr	Lys	Pro	Gln	
			625					630					635			
gga	ttc	aaa	tac	aaa	agt	gga	cag	ttc	atg	ttg	gtg	aac	tgc	cga	gcc	2090
Gly	Phe	Lys	Tyr	Lys	Ser	Gly	Gln	Phe	Met	Leu	Val	Asn	Cys	Arg	Ala	
		640					645					650				
gta	tct	cca	ttc	gaa	tgg	cat	cct	ttc	tca	atc	aca	tca	gct	ccc	gga	2138
Val	Ser	Pro	Phe	Glu	Trp	His	Pro	Phe	Ser	Ile	Thr	Ser	Ala	Pro	Gly	
	655					660					665					
gac	gat	tac	ctg	agc	gta	cat	atc	cgc	act	ctc	ggt	gac	tgg	aca	cgt	2186
Asp	Asp	Tyr	Leu	Ser	Val	His	Ile	Arg	Thr	Leu	Gly	Asp	Trp	Thr	Arg	
670					675					680					685	
aag	ctc	agg	acc	gtt	ttc	tcc	gag	gtt	tgc	aaa	cct	cct	acc	gcc	ggt	2234
Lys	Leu	Arg	Thr	Val	Phe	Ser	Glu	Val	Cys	Lys	Pro	Pro	Thr	Ala	Gly	
			690					695						700		
aaa	agc	ggt	ctt	ctc	cga	gca	gac	gga	gga	gat	gga	aac	ctc	ccg	ttc	2282
Lys	Ser	Gly	Leu	Leu	Arg	Ala	Asp	Gly	Gly	Asp	Gly	Asn	Leu	Pro	Phe	
		705						710					715			
ccg	aag	gtc	ctt	atc	gac	ggt	cca	tac	ggt	gct	ccc	gca	caa	gac	tac	2330
Pro	Lys	Val	Leu	Ile	Asp	Gly	Pro	Tyr	Gly	Ala	Pro	Ala	Gln	Asp	Tyr	
		720					725					730				
aag	aaa	tac	gac	gtg	gta	ctc	ctc	gta	ggt	ctc	ggc	att	gga	gcc	acg	2378
Lys	Lys	Tyr	Asp	Val	Val	Leu	Leu	Val	Gly	Leu	Gly	Ile	Gly	Ala	Thr	
	735					740					745					
cct	atg	atc	agt	atc	ctt	aag	gac	atc	atc	aac	aac	atg	aaa	ggt	cct	2426
Pro	Met	Ile	Ser	Ile	Leu	Lys	Asp	Ile	Ile	Asn	Asn	Met	Lys	Gly	Pro	
750					755					760					765	
gac	cgc	gac	agc	gac	att	gag	aac	aat	aac	agt	aac	aac	aat	agt	aaa	2474
Asp	Arg	Asp	Ser	Asp	Ile	Glu	Asn	Asn	Asn	Ser	Asn	Asn	Asn	Asn	Lys	
			770					775						780		
ggg	ttt	aag	aca	agg	aaa	gct	tat	ttc	tac	tgg	gtg	act	agg	gaa	caa	2522
Gly	Phe	Lys	Thr	Arg	Lys	Ala	Tyr	Phe	Tyr	Trp	Val	Thr	Arg	Glu	Gln	
		785					790						795			
gga	tca	ttc	gag	tgg	ttc	aag	gga	ata	atg	gac	gag	att	tcg	gag	tta	2570
Gly	Ser	Phe	Glu	Trp	Phe	Lys	Gly	Ile	Met	Asp	Glu	Ile	Ser	Glu	Leu	
		800					805					810				
gac	gag	gaa	gga	atc	atc	gag	ctt	cac	aat	tat	tgc	acg	agt	gtg	tac	2618
Asp	Glu	Glu	Gly	Ile	Ile	Glu	Leu	His	Asn	Tyr	Cys	Thr	Ser	Val	Tyr	
	815					820					825					
gag	gaa	ggt	gat	gca	aga	gtg	gct	ctc	att	gcc	atg	ctt	cag	tcg	ttg	2666
Glu	Glu	Gly	Asp	Ala	Arg	Val	Ala	Leu	Ile	Ala	Met	Leu	Gln	Ser	Leu	
830					835					840					845	
caa	cac	gct	aag	aac	ggt	gtg	gat	gtt	gtg	tcg	ggt	aca	cgt	gtc	aag	2714
Gln	His	Ala	Lys	Asn	Gly	Val	Asp	Val	Val	Ser	Gly	Thr	Arg	Val	Lys	
			850					855						860		
tcc	cac	ttc	gct	aaa	cct	aac	tgg	aga	caa	gtc	tac	aag	aag	atc	gct	2762
Ser	His	Phe	Ala	Lys	Pro	Asn	Trp	Arg	Gln	Val	Tyr	Lys	Lys	Ile	Ala	
		865					870						875			
gtt	caa	cat	ccc	ggc	aaa	aga	ata	gga	gtc	ttc	tac	tgt	gga	atg	cca	2810
Val	Gln	His	Pro	Gly	Lys	Arg	Ile	Gly	Val	Phe	Tyr	Cys	Gly	Met	Pro	
		880					885					890				
gga	atg	ata	aag	gaa	tta	aaa	aat	cta	gct	ttg	gat	ttt	tct	cga	aag	2858
Gly	Met	Ile	Lys	Glu	Leu	Lys	Asn	Leu	Ala	Leu	Asp	Phe	Ser	Arg	Lys	
	895					900					905					
aca	act	acc	aag	ttt	gac	ttc	cac	aaa	gag	aac	ttc	tagattaatt				2904

Thr Thr Thr Lys Phe Asp Phe His Lys Glu Asn Phe  
 910 915 920  
 atatacgttg tagaaaaata aaacaagaaa caactataca aataaatatt ttttttaa 2964  
 tcttttcatt ttatgtaaaa ttatctgagt tatctttttt tgtaaaaaaa aaaaaaaaaa 3024  
 aaaaaaaaaa a 3035

<210> 14  
 <211> 921  
 <212> PRT  
 <213> Arabidopsis thaliana

<400> 14  
 Met Lys Met Arg Arg Gly Asn Ser Ser Asn Asp His Glu Leu Gly Ile  
 1 5 10 15  
 Leu Arg Gly Ala Asn Ser Asp Thr Asn Ser Asp Thr Glu Ser Ile Ala  
 20 25 30  
 Ser Asp Arg Gly Ala Phe Ser Gly Pro Leu Gly Arg Pro Lys Arg Ala  
 35 40 45  
 Ser Lys Lys Asn Ala Arg Phe Ala Asp Asp Leu Pro Lys Arg Ser Asn  
 50 55 60  
 Ser Val Ala Gly Gly Arg Gly Asp Asp Asp Glu Tyr Val Glu Ile Thr  
 65 70 75 80  
 Leu Asp Ile Arg Asp Asp Ser Val Ala Val His Ser Val Gln Gln Ala  
 85 90 95  
 Ala Gly Gly Gly Gly His Leu Glu Asp Pro Glu Leu Ala Leu Leu Thr  
 100 105 110  
 Lys Lys Thr Leu Glu Ser Ser Leu Asn Asn Thr Thr Ser Leu Ser Phe  
 115 120 125  
 Phe Arg Ser Thr Ser Ser Arg Ile Lys Asn Ala Ser Arg Glu Leu Arg  
 130 135 140  
 Arg Val Phe Ser Arg Arg Pro Ser Pro Ala Val Arg Arg Phe Asp Arg  
 145 150 155 160  
 Thr Ser Ser Ala Ala Ile His Ala Leu Lys Gly Leu Lys Phe Ile Ala  
 165 170 175  
 Thr Lys Thr Ala Ala Trp Pro Ala Val Asp Gln Arg Phe Asp Lys Leu  
 180 185 190  
 Ser Ala Asp Ser Asn Gly Leu Leu Ser Ala Lys Phe Trp Glu Cys  
 195 200 205  
 Leu Gly Met Asn Lys Glu Ser Lys Asp Phe Ala Asp Gln Leu Phe Arg  
 210 215 220  
 Ala Leu Ala Arg Arg Asn Asn Val Ser Gly Asp Ala Ile Thr Lys Glu  
 225 230 235 240  
 Gln Leu Arg Ile Phe Trp Glu Gln Ile Ser Asp Glu Ser Phe Asp Ala  
 245 250 255  
 Lys Leu Gln Val Phe Phe Asp Met Val Asp Lys Asp Glu Asp Gly Arg  
 260 265 270  
 Val Thr Glu Glu Glu Val Ala Glu Ile Ile Ser Leu Ser Ala Ser Ala  
 275 280 285  
 Asn Lys Leu Ser Asn Ile Gln Lys Gln Ala Lys Glu Tyr Ala Ala Leu  
 290 295 300  
 Ile Met Glu Glu Leu Asp Pro Asp Asn Ala Gly Phe Ile Met Ile Glu  
 305 310 315 320  
 Asn Leu Glu Met Leu Leu Gln Ala Pro Asn Gln Ser Val Arg Met  
 325 330 335  
 Gly Asp Ser Arg Ile Leu Ser Gln Met Leu Ser Gln Lys Leu Arg Pro  
 340 345 350  
 Ala Lys Glu Ser Asn Pro Leu Leu Arg Trp Ser Glu Lys Ile Lys Tyr  
 355 360 365  
 Phe Ile Leu Asp Asn Trp Gln Arg Leu Trp Ile Met Met Leu Trp Leu  
 370 375 380  
 Gly Ile Cys Gly Gly Leu Phe Thr Tyr Lys Phe Ile Gln Tyr Lys Asn

385					390					395					400
Lys	Ala	Ala	Tyr	Gly	Val	Met	Gly	Tyr	Cys	Val	Cys	Val	Ala	Lys	Gly
				405					410					415	
Gly	Ala	Glu	Thr	Leu	Lys	Phe	Asn	Met	Ala	Leu	Ile	Leu	Leu	Pro	Val
			420					425					430		
Cys	Arg	Asn	Thr	Ile	Thr	Trp	Leu	Arg	Asn	Lys	Thr	Lys	Leu	Gly	Thr
		435					440					445			
Val	Val	Pro	Phe	Asp	Asp	Ser	Leu	Asn	Phe	His	Lys	Val	Ile	Ala	Ser
	450					455					460				
Gly	Ile	Val	Val	Gly	Val	Leu	Leu	His	Ala	Gly	Ala	His	Leu	Thr	Cys
465					470					475					480
Asp	Phe	Pro	Arg	Leu	Ile	Ala	Ala	Asp	Glu	Asp	Thr	Tyr	Glu	Pro	Met
			485						490					495	
Glu	Lys	Tyr	Phe	Gly	Asp	Gln	Pro	Thr	Ser	Tyr	Trp	Trp	Phe	Val	Lys
			500					505					510		
Gly	Val	Glu	Gly	Trp	Thr	Gly	Ile	Val	Met	Val	Val	Leu	Met	Ala	Ile
		515					520					525			
Ala	Phe	Thr	Leu	Ala	Thr	Pro	Trp	Phe	Arg	Arg	Asn	Lys	Leu	Asn	Leu
	530					535					540				
Pro	Asn	Phe	Leu	Lys	Lys	Leu	Thr	Gly	Phe	Asn	Ala	Phe	Trp	Tyr	Thr
545					550					555					560
His	His	Leu	Phe	Ile	Ile	Val	Tyr	Ala	Leu	Leu	Ile	Val	His	Gly	Ile
			565						570					575	
Lys	Leu	Tyr	Leu	Thr	Lys	Ile	Trp	Tyr	Gln	Lys	Thr	Thr	Trp	Met	Tyr
		580						585					590		
Leu	Ala	Val	Pro	Ile	Leu	Leu	Tyr	Ala	Ser	Glu	Arg	Leu	Leu	Arg	Ala
		595					600					605			
Phe	Arg	Ser	Ser	Ile	Lys	Pro	Val	Lys	Met	Ile	Lys	Val	Ala	Val	Tyr
	610					615					620				
Pro	Gly	Asn	Val	Leu	Ser	Leu	His	Met	Thr	Lys	Pro	Gln	Gly	Phe	Lys
625					630					635					640
Tyr	Lys	Ser	Gly	Gln	Phe	Met	Leu	Val	Asn	Cys	Arg	Ala	Val	Ser	Pro
			645						650					655	
Phe	Glu	Trp	His	Pro	Phe	Ser	Ile	Thr	Ser	Ala	Pro	Gly	Asp	Asp	Tyr
		660						665					670		
Leu	Ser	Val	His	Ile	Arg	Thr	Leu	Gly	Asp	Trp	Thr	Arg	Lys	Leu	Arg
		675					680					685			
Thr	Val	Phe	Ser	Glu	Val	Cys	Lys	Pro	Pro	Thr	Ala	Gly	Lys	Ser	Gly
	690					695					700				
Leu	Leu	Arg	Ala	Asp	Gly	Gly	Asp	Gly	Asn	Leu	Pro	Phe	Pro	Lys	Val
705					710					715					720
Leu	Ile	Asp	Gly	Pro	Tyr	Gly	Ala	Pro	Ala	Gln	Asp	Tyr	Lys	Lys	Tyr
			725						730					735	
Asp	Val	Val	Leu	Val	Gly	Leu	Gly	Ile	Gly	Ala	Thr	Pro	Met	Ile	
		740					745					750			
Ser	Ile	Leu	Lys	Asp	Ile	Ile	Asn	Asn	Met	Lys	Gly	Pro	Asp	Arg	Asp
		755					760					765			
Ser	Asp	Ile	Glu	Asn	Asn	Asn	Ser	Asn	Asn	Asn	Ser	Lys	Gly	Phe	Lys
	770					775					780				
Thr	Arg	Lys	Ala	Tyr	Phe	Tyr	Trp	Val	Thr	Arg	Glu	Gln	Gly	Ser	Phe
785					790					795					800
Glu	Trp	Phe	Lys	Gly	Ile	Met	Asp	Glu	Ile	Ser	Glu	Leu	Asp	Glu	Glu
			805						810					815	
Gly	Ile	Ile	Glu	Leu	His	Asn	Tyr	Cys	Thr	Ser	Val	Tyr	Glu	Glu	Gly
			820					825					830		
Asp	Ala	Arg	Val	Ala	Leu	Ile	Ala	Met	Leu	Gln	Ser	Leu	Gln	His	Ala
		835					840					845			
Lys	Asn	Gly	Val	Asp	Val	Val	Ser	Gly	Thr	Arg	Val	Lys	Ser	His	Phe
	850					855					860				
Ala	Lys	Pro	Asn	Trp	Arg	Gln	Val	Tyr	Lys	Lys	Ile	Ala	Val	Gln	His
865					870					875					880



Pro	Gly	Lys	Arg	Ile	Gly	Val	Phe	Tyr	Cys	Gly	Met	Pro	Gly	Met	Ile
				885					890					895	
Lys	Glu	Leu	Lys	Asn	Leu	Ala	Leu	Asp	Phe	Ser	Arg	Lys	Thr	Thr	Thr
			900					905					910		
Lys	Phe	Asp	Phe	His	Lys	Glu	Asn	Phe							
		915					920								

```
<210> 15
<211> 3338
<212> DNA
<213> Nicotiana tabacum
```

```
<220>
<221> CDS
<222> (313)..(3129)
<223> coding for NADPH oxidase
```

```
<220>
<221> misc_feature
<222> (1952)..(1952)
<223> n is a, c, g, or t
```

<400> 15																
ggc		cac		gag		aaa		aat		cgc		aac		gaa		60
gaa		aga		aag		cag		aac		gac		caa		aat		120
ata		cca		atta		tta		atc		tct		cgc		gac		180
aca		tct		ttt		tct		tct		cgc		gac		aat		240
gtt		cact		act		tca		aaa		gac		aat		gaa		300
aaa		act		tat		ag		aa		tgc		gaa		aat		351
		Met		Gln		Asn		Ser		Glu		Asn		His		
		1		5		10										
cac		cat		tcg		gac		aca		gag		ata		att		399
His		His		Ser		Asp		Thr		Glu		Ile		Ile		
		15						20						25		
ggt		ccg		tta		agc		gga		ccg		tta		aac		447
Gly		Pro		Leu		Ser		Gly		Pro		Leu		Asn		
		30						35						40		
aga		ttt		aac		att		cct		gaa		tct		acc		495
Arg		Phe		Asn		Ile		Pro		Glu		Ser		Thr		
				50								55				
ggc		ggc		aag		tcc		aat		gat		gat		gcg		543
Gly		Gly		Lys		Ser		Asn		Asp		Asp		Ala		
				65						70				75		
cgc		gaa		gat		tcc		gtc		gct		gtc		cac		591
Arg		Glu		Asp		Ser		Val		Ala		Val		His		
		80						85						90		
gac		gtg		gaa		gat		ccc		gag		ctg		gct		639
Asp		Val		Glu		Asp		Pro		Glu		Leu		Ala		
		95						100						105		
aag		tcc		act		tta		gga		tct		tca		ctt		687
Lys		Ser		Thr		Leu		Gly		Ser		Ser		Leu		
		110						115						120		
cgc		caa		gtg		tca		caa		gag		ctc		agg		735
Arg		Gln		Val		Ser		Gln		Glu		Leu		Arg		
				130						135				140		
cca		att		cct		act		gga		agg		ttc		gac		783
Pro		Ile		Pro		Thr		Gly		Arg		Phe		Asp		
		145						150						155		
gct		ctt		aaa		ggt		ctc		aag		ttt		att		831
Ala		Leu		Lys		Gly		Leu		Lys		Phe		Ile		
		160						165						170		

tgg	gcc	gcc	gtc	gag	aag	cgg	ttc	gat	gag	att	act	gct	tct	act	act	879
Trp	Ala	Ala	Val	Glu	Lys	Arg	Phe	Asp	Glu	Ile	Thr	Ala	Ser	Thr	Thr	
175						180					185					
ggt	ttg	ctt	cct	cgt	gcc	aaa	ttt	gga	gaa	tgt	ata	ggt	atg	aat	aag	927
Gly	Leu	Leu	Pro	Arg	Ala	Lys	Phe	Gly	Glu	Cys	Ile	Gly	Met	Asn	Lys	
190					195					200					205	
gag	tct	aag	gaa	ttt	gct	gtt	gag	cta	tat	gat	gcg	cta	gct	cgg	agg	975
Glu	Ser	Lys	Glu	Phe	Ala	Val	Glu	Leu	Tyr	Asp	Ala	Leu	Ala	Arg	Arg	
				210					215					220		
aga	aac	att	aca	act	gat	tcc	att	aac	aaa	gca	cag	ctc	aaa	gag	ttc	1023
Arg	Asn	Ile	Thr	Thr	Asp	Ser	Ile	Asn	Lys	Ala	Gln	Leu	Lys	Glu	Phe	
		225					230						235			
tgg	gac	caa	gtg	gct	gac	caa	agt	ttt	gat	tct	cgc	ctt	caa	aca	ttt	1071
Trp	Asp	Gln	Val	Ala	Asp	Gln	Ser	Phe	Asp	Ser	Arg	Leu	Gln	Thr	Phe	
		240					245					250				
ttt	gac	atg	gtt	gat	aaa	gat	gct	gat	ggt	aga	att	aca	gaa	gaa	gaa	1119
Phe	Asp	Met	Val	Asp	Lys	Asp	Ala	Asp	Gly	Arg	Ile	Thr	Glu	Glu	Glu	
	255					260					265					
gtc	aga	gag	att	ata	ggc	ctt	agc	gcg	tcg	gcc	aac	agg	ctg	tca	aca	1167
Val	Arg	Glu	Ile	Ile	Gly	Leu	Ser	Ala	Ser	Ala	Asn	Arg	Leu	Ser	Thr	
270					275					280					285	
atc	cag	aaa	caa	gct	gat	gaa	tac	gca	gca	atg	atc	atg	gaa	gag	ttg	1215
Ile	Gln	Lys	Gln	Ala	Asp	Glu	Tyr	Ala	Ala	Met	Ile	Met	Glu	Glu	Leu	
				290				295					300			
gat	cct	aac	aac	ctc	gga	tac	att	atg	att	gag	aac	ttg	gaa	atg	ctt	1263
Asp	Pro	Asn	Asn	Leu	Gly	Tyr	Ile	Met	Ile	Glu	Asn	Leu	Glu	Met	Leu	
		305					310					315				
tta	ctg	caa	gca	cca	aat	caa	tca	gtg	caa	aga	gga	ggc	gaa	agt	cgg	1311
Leu	Leu	Gln	Ala	Pro	Asn	Gln	Ser	Val	Gln	Arg	Gly	Gly	Glu	Ser	Arg	
		320				325						330				
aac	ttg	agt	caa	atg	cta	agt	caa	aaa	cta	aag	cat	aca	caa	gag	aga	1359
Asn	Leu	Ser	Gln	Met	Leu	Ser	Gln	Lys	Leu	Lys	His	Thr	Gln	Glu	Arg	
	335					340					345					
aat	cca	ata	gta	aga	tgg	tac	aag	agt	ttc	atg	tac	ttt	ttg	ctg	gat	1407
Asn	Pro	Ile	Val	Arg	Trp	Tyr	Lys	Ser	Phe	Met	Tyr	Phe	Leu	Leu	Asp	
350					355					360					365	
aat	tgg	caa	aga	gtt	tgg	gta	ttg	tta	ctg	tgg	att	gga	att	atg	gct	1455
Asn	Trp	Gln	Arg	Val	Trp	Val	Leu	Leu	Leu	Trp	Ile	Gly	Ile	Met	Ala	
				370				375					380			
ggt	cta	ttt	aca	tgg	aaa	tat	ata	cag	tat	aaa	gaa	aaa	gct	gca	tat	1503
Gly	Leu	Phe	Thr	Trp	Lys	Tyr	Ile	Gln	Tyr	Lys	Glu	Lys	Ala	Ala	Tyr	
		385					390					395				
aaa	gtc	atg	ggt	ccc	tgt	gtg	tgt	ttt	gcc	aaa	ggt	gct	gct	gaa	aca	1551
Lys	Val	Met	Gly	Pro	Cys	Val	Cys	Phe	Ala	Lys	Gly	Ala	Ala	Glu	Thr	
	400					405					410					
ctc	aag	ctc	aac	atg	gca	att	att	tta	ttt	ccg	gtt	tgc	aga	aac	acg	1599
Leu	Lys	Leu	Asn	Met	Ala	Ile	Ile	Leu	Phe	Pro	Val	Cys	Arg	Asn	Thr	
	415				420						425					
atc	aca	tgg	ctt	cga	aat	aag	acc	aga	tta	ggt	gct	gct	ggt	cct	ttt	1647
Ile	Thr	Trp	Leu	Arg	Asn	Lys	Thr	Arg	Leu	Gly	Ala	Ala	Val	Pro	Phe	
430					435					440					445	
gat	gat	aac	ctt	aat	ttt	cac	aaa	gtg	ata	gca	gtg	gca	att	gct	ctt	1695
Asp	Asp	Asn	Leu	Asn	Phe	His	Lys	Val	Ile	Ala	Val	Ala	Ile	Ala	Leu	
				450				455					460			
ggg	gtt	gga	ata	cac	gga	cta	tct	cac	ttg	aca	tgt	gat	ttt	cct	cgg	1743
Gly	Val	Gly	Ile	His	Gly	Leu	Ser	His	Leu	Thr	Cys	Asp	Phe	Pro	Arg	
		465				470						475				
ctt	tta	aat	gct	agt	gaa	gaa	gaa	tat	gaa	cca	atg	aag	tac	tat	ttt	1791
Leu	Leu	Asn	Ala	Ser	Glu	Glu	Glu	Tyr	Glu	Pro	Met	Lys	Tyr	Tyr	Phe	
		480				485						490				
gga	gat	cag	cca	gaa	agc	tat	tgg	tgg	ttt	ata	aaa	gga	gta	gaa	ggg	1839

Gly	Asp	Gln	Pro	Glu	Ser	Tyr	Trp	Trp	Phe	Ile	Lys	Gly	Val	Glu	Gly	
495						500					505					
gta	act	gga	att	ata	atg	gtg	gtt	tta	atg	gca	ata	gca	ttt	act	cta	1887
Val	Thr	Gly	Ile	Ile	Met	Val	Val	Leu	Met	Ala	Ile	Ala	Phe	Thr	Leu	
510					515					520					525	
gca	acc	cca	tgg	ttt	aga	agg	aat	aga	gtt	agt	ttg	cca	aaa	cca	ttt	1935
Ala	Thr	Pro	Trp	Phe	Arg	Arg	Asn	Arg	Val	Ser	Leu	Pro	Lys	Pro	Phe	
				530					535					540		
cac	aaa	ctc	act	gga	tnt	aat	gcc	ttt	tgg	tac	tct	cac	cat	ctc	ttt	1983
His	Lys	Leu	Thr	Gly	Xaa	Asn	Ala	Phe	Trp	Tyr	Ser	His	His	Leu	Phe	
			545				550						555			
gtt	atc	gtc	tac	act	ctg	ttc	att	gtg	cat	ggt	gaa	aag	cta	tac	att	2031
Val	Ile	Val	Tyr	Thr	Leu	Phe	Ile	Val	His	Gly	Glu	Lys	Leu	Tyr	Ile	
		560					565					570				
acc	aaa	gat	tgg	tac	aag	aga	acc	gac	atg	gat	gta	ctt	tta	act	atc	2079
Thr	Lys	Asp	Trp	Tyr	Lys	Arg	Thr	Asp	Met	Asp	Val	Leu	Leu	Thr	Ile	
	575					580					585					
cca	atc	ata	ctc	tat	gct	agt	gaa	agg	ttg	att	agg	gca	ttc	agg	tca	2127
Pro	Ile	Ile	Leu	Tyr	Ala	Ser	Glu	Arg	Leu	Ile	Arg	Ala	Phe	Arg	Ser	
590					595					600					605	
agc	att	aaa	gct	gtt	aag	att	ttg	aag	gtg	gca	gta	tat	cca	gga	aat	2175
Ser	Ile	Lys	Ala	Val	Lys	Ile	Leu	Lys	Val	Ala	Val	Tyr	Pro	Gly	Asn	
			610						615					620		
gtg	ttg	gca	ctt	cac	atg	tca	aaa	cca	cag	ggc	tac	aaa	tac	aaa	agt	2223
Val	Leu	Ala	Leu	His	Met	Ser	Lys	Pro	Gln	Gly	Tyr	Lys	Tyr	Lys	Ser	
			625					630					635			
ggg	caa	tac	atg	ttt	gtc	aac	tgt	gct	gca	gtt	tct	cca	ttt	gag	tgg	2271
Gly	Gln	Tyr	Met	Phe	Val	Asn	Cys	Ala	Ala	Val	Ser	Pro	Phe	Glu	Trp	
		640				645						650				
cat	cca	ttt	tca	att	act	tcg	gcc	cca	gga	gat	gac	tat	ctc	agt	gtc	2319
His	Pro	Phe	Ser	Ile	Thr	Ser	Ala	Pro	Gly	Asp	Asp	Tyr	Leu	Ser	Val	
		655				660					665					
cat	att	cga	act	ctt	ggt	gat	tgg	acc	agg	caa	ctt	aaa	act	gtt	ttc	2367
His	Ile	Arg	Thr	Leu	Gly	Asp	Trp	Thr	Arg	Gln	Leu	Lys	Thr	Val	Phe	
670					675					680					685	
tcc	gag	gtt	tgc	cag	cca	cca	cct	aat	gga	aaa	agt	gga	ctc	ctc	aga	2415
Ser	Glu	Val	Cys	Gln	Pro	Pro	Pro	Asn	Gly	Lys	Ser	Gly	Leu	Leu	Arg	
			690						695					700		
gct	gac	tac	ttg	caa	gga	gag	aat	aat	cct	aat	ttc	cca	agg	gtg	tta	2463
Ala	Asp	Tyr	Leu	Gln	Gly	Glu	Asn	Asn	Pro	Asn	Phe	Pro	Arg	Val	Leu	
			705				710						715			
ata	gat	gga	cca	tat	gga	gca	cca	gca	caa	gac	tac	aag	aaa	tat	gag	2511
Ile	Asp	Gly	Pro	Tyr	Gly	Ala	Pro	Ala	Gln	Asp	Tyr	Lys	Lys	Tyr	Glu	
		720					725						730			
gtg	gtt	ttg	ttg	gta	ggt	ctt	gga	att	gga	gct	aca	cca	atg	atc	agt	2559
Val	Val	Leu	Leu	Val	Gly	Leu	Gly	Ile	Gly	Ala	Thr	Pro	Met	Ile	Ser	
		735				740					745					
att	gtt	aaa	gac	att	gtc	aac	aac	atg	aag	gca	atg	gac	gaa	gaa	gaa	2607
Ile	Val	Lys	Asp	Ile	Val	Asn	Asn	Met	Lys	Ala	Met	Asp	Glu	Glu	Glu	
					755					760					765	
aat	tcc	ttg	gaa	gat	gga	cac	aat	aat	aat	atg	gca	cca	aat	tct	agc	2655
Asn	Ser	Leu	Glu	Asp	Gly	His	Asn	Asn	Asn	Met	Ala	Pro	Asn	Ser	Ser	
				770						775				780		
ccc	aat	att	gca	aaa	aat	aag	ggt	aat	aaa	tca	ggt	tca	gca	agt	gga	2703
Pro	Asn	Ile	Ala	Lys	Asn	Lys	Gly	Asn	Lys	Ser	Gly	Ser	Ala	Ser	Gly	
			785					790					795			
gga	aat	aat	ttc	aat	aca	agg	aga	gca	tat	ttc	tat	tgg	gtt	act	aga	2751
Gly	Asn	Asn	Phe	Asn	Thr	Arg	Arg	Ala	Tyr	Phe	Tyr	Trp	Val	Thr	Arg	
		800					805					810				
gaa	caa	ggt	tca	ttt	gat	tgg	ttc	aaa	ggt	ata	atg	aat	gaa	gct	gct	2799
Glu	Gln	Gly	Ser	Phe	Asp	Trp	Phe	Lys	Gly	Ile	Met	Asn	Glu	Ala	Ala	

```

      815              820              825
gaa atg gac cat aag gga gta att gaa atg cat aat tat tgt act agt 2847
Glu Met Asp His Lys Gly Val Ile Glu Met His Asn Tyr Cys Thr Ser
830              835              840              845
gtt tat gaa gaa ggt gat gct cgt tct gct ctt att act atg ctt cag 2895
Val Tyr Glu Glu Gly Asp Ala Arg Ser Ala Leu Ile Thr Met Leu Gln
      850              855              860
tct ctt cac cat gcc aaa aat ggt gtt gac att gtc tct ggc acc aga 2943
Ser Leu His His Ala Lys Asn Gly Val Asp Ile Val Ser Gly Thr Arg
      865              870              875
gtt aag tca cat ttt gct aaa cct aat tgg cgt aat gtc tac aaa cgc 2991
Val Lys Ser His Phe Ala Lys Pro Asn Trp Arg Asn Val Tyr Lys Arg
      880              885              890
att gct ctc aac cac cct gag gct aaa gtt ggg gtc ttc tat tgt ggg 3039
Ile Ala Leu Asn His Pro Glu Ala Lys Val Gly Val Phe Tyr Cys Gly
      895              900              905
gca cca gca ctg acc aaa gaa cta aga caa cac gcc ttg gat ttt tca 3087
Ala Pro Ala Leu Thr Lys Glu Leu Arg Gln His Ala Leu Asp Phe Ser
910              915              920              925
cac aag aca tct acc aag ttt gat ttc cat aaa gaa aat ttt 3129
His Lys Thr Ser Thr Lys Phe Asp Phe His Lys Glu Asn Phe
      930              935
tgagcaaaga atagaccatt aagcagagca ttaaaatttc atcaaaacag ctaaggacac 3189
aggttggttt atagaagtct accaactctc cctattgtgt acagataatg ttgcacttca 3249
agttgatata tagttgtggt tgtgatgcta gtatattaca aaataataag attattttta 3309
ttttagtagtaa aaaaaaaaaa aaaaaaaaaa 3338

```

<210> 16

<211> 939

<212> PRT

<213> Nicotiana tabacum

<220>

<221> misc\_feature

<222> (547)..(547)

<223> The 'Xaa' at location 547 stands for Tyr, Cys, Ser, or Phe.

<400> 16

```

Met Gln Asn Ser Glu Asn His His Pro His His Gln His His His Ser
 1              5              10              15
Asp Thr Glu Ile Ile Gly Asn Asp Arg Ala Ser Tyr Ser Gly Pro Leu
      20              25              30
Ser Gly Pro Leu Asn Lys Arg Gly Gly Lys Lys Ser Ala Arg Phe Asn
      35              40              45
Ile Pro Glu Ser Thr Asp Ile Gly Thr Ser Val Gly Thr Gly Gly Lys
      50              55              60
Ser Asn Asp Asp Ala Tyr Val Glu Ile Thr Leu Asp Val Arg Glu Asp
      65              70              75              80
Ser Val Ala Val His Ser Val Lys Thr Ala Gly Gly Asp Asp Val Glu
      85              90              95
Asp Pro Glu Leu Ala Leu Leu Ala Lys Gly Leu Glu Lys Lys Ser Thr
      100              105              110
Leu Gly Ser Ser Leu Val Arg Asn Ala Ser Ser Arg Ile Arg Gln Val
      115              120              125
Ser Gln Glu Leu Arg Arg Leu Ala Ser Leu Asn Lys Arg Pro Ile Pro
      130              135              140
Thr Gly Arg Phe Asp Arg Asn Lys Ser Ala Ala Ala His Ala Leu Lys
      145              150              155              160
Gly Leu Lys Phe Ile Ser Lys Thr Asp Gly Gly Ala Gly Trp Ala Ala
      165              170              175
Val Glu Lys Arg Phe Asp Glu Ile Thr Ala Ser Thr Thr Gly Leu Leu

```

			180						185						190					
Pro	Arg	Ala	Lys	Phe	Gly	Glu	Cys	Ile	Gly	Met	Asn	Lys	Glu	Ser	Lys					
		195					200					205								
Glu	Phe	Ala	Val	Glu	Leu	Tyr	Asp	Ala	Leu	Ala	Arg	Arg	Arg	Asn	Ile					
	210					215					220									
Thr 225	Thr	Asp	Ser	Ile	Asn	Lys	Ala	Gln	Leu	Lys	Glu	Phe	Trp	Asp	Gln 240					
					230					235										
Val	Ala	Asp	Gln	Ser	Phe	Asp	Ser	Arg	Leu	Gln	Thr	Phe	Phe	Asp	Met					
					245				250					255						
Val	Asp	Lys	Asp	Ala	Asp	Gly	Arg	Ile	Thr	Glu	Glu	Glu	Val	Arg	Glu					
					260			265					270							
Ile	Ile	Gly	Leu	Ser	Ala	Ser	Ala	Asn	Arg	Leu	Ser	Thr	Ile	Gln	Lys					
		275					280					285								
Gln	Ala	Asp	Glu	Tyr	Ala	Ala	Met	Ile	Met	Glu	Glu	Leu	Asp	Pro	Asn					
	290					295				300										
Asn 305	Leu	Gly	Tyr	Ile	Met	Ile	Glu	Asn	Leu	Glu	Met	Leu	Leu	Leu	Gln 320					
					310					315										
Ala	Pro	Asn	Gln	Ser	Val	Gln	Arg	Gly	Gly	Glu	Ser	Arg	Asn	Leu	Ser					
					325				330					335						
Gln	Met	Leu	Ser	Gln	Lys	Leu	Lys	His	Thr	Gln	Glu	Arg	Asn	Pro	Ile					
					340			345					350							
Val	Arg	Trp	Tyr	Lys	Ser	Phe	Met	Tyr	Phe	Leu	Leu	Asp	Asn	Trp	Gln					
							360					365								
Arg	Val	Trp	Val	Leu	Leu	Leu	Trp	Ile	Gly	Ile	Met	Ala	Gly	Leu	Phe					
	370					375				380										
Thr 385	Trp	Lys	Tyr	Ile	Gln	Tyr	Lys	Glu	Lys	Ala	Ala	Tyr	Lys	Val	Met 400					
					390					395										
Gly	Pro	Cys	Val	Cys	Phe	Ala	Lys	Gly	Ala	Ala	Glu	Thr	Leu	Lys	Leu					
				405					410				415							
Asn	Met	Ala	Ile	Ile	Leu	Phe	Pro	Val	Cys	Arg	Asn	Thr	Ile	Thr	Trp					
					420			425					430							
Leu	Arg	Asn	Lys	Thr	Arg	Leu	Gly	Ala	Ala	Val	Pro	Phe	Asp	Asp	Asn					
		435					440					445								
Leu	Asn	Phe	His	Lys	Val	Ile	Ala	Val	Ala	Ile	Ala	Leu	Gly	Val	Gly					
	450					455				460										
Ile 465	His	Gly	Leu	Ser	His	Leu	Thr	Cys	Asp	Phe	Pro	Arg	Leu	Leu	Asn 480					
					470					475										
Ala	Ser	Glu	Glu	Glu	Tyr	Glu	Pro	Met	Lys	Tyr	Tyr	Phe	Gly	Asp	Gln					
					485				490					495						
Pro	Glu	Ser	Tyr	Trp	Trp	Phe	Ile	Lys	Gly	Val	Glu	Gly	Val	Thr	Gly					
					500			505					510							
Ile	Ile	Met	Val	Val	Leu	Met	Ala	Ile	Ala	Phe	Thr	Leu	Ala	Thr	Pro					
		515					520				</									

Thr Leu Gly Asp Trp Thr Arg Gln Leu Lys Thr Val Phe Ser Glu Val  
 675 680 685  
 Cys Gln Pro Pro Pro Asn Gly Lys Ser Gly Leu Leu Arg Ala Asp Tyr  
 690 695 700  
 Leu Gln Gly Glu Asn Asn Pro Asn Phe Pro Arg Val Leu Ile Asp Gly  
 705 710 715 720  
 Pro Tyr Gly Ala Pro Ala Gln Asp Tyr Lys Lys Tyr Glu Val Val Leu  
 725 730 735  
 Leu Val Gly Leu Gly Ile Gly Ala Thr Pro Met Ile Ser Ile Val Lys  
 740 745 750  
 Asp Ile Val Asn Asn Met Lys Ala Met Asp Glu Glu Glu Asn Ser Leu  
 755 760 765  
 Glu Asp Gly His Asn Asn Asn Met Ala Pro Asn Ser Ser Pro Asn Ile  
 770 775 780  
 Ala Lys Asn Lys Gly Asn Lys Ser Gly Ser Ala Ser Gly Gly Asn Asn  
 785 790 795 800  
 Phe Asn Thr Arg Arg Ala Tyr Phe Tyr Trp Val Thr Arg Glu Gln Gly  
 805 810 815  
 Ser Phe Asp Trp Phe Lys Gly Ile Met Asn Glu Ala Ala Glu Met Asp  
 820 825 830  
 His Lys Gly Val Ile Glu Met His Asn Tyr Cys Thr Ser Val Tyr Glu  
 835 840 845  
 Glu Gly Asp Ala Arg Ser Ala Leu Ile Thr Met Leu Gln Ser Leu His  
 850 855 860  
 His Ala Lys Asn Gly Val Asp Ile Val Ser Gly Thr Arg Val Lys Ser  
 865 870 875 880  
 His Phe Ala Lys Pro Asn Trp Arg Asn Val Tyr Lys Arg Ile Ala Leu  
 885 890 895  
 Asn His Pro Glu Ala Lys Val Gly Val Phe Tyr Cys Gly Ala Pro Ala  
 900 905 910  
 Leu Thr Lys Glu Leu Arg Gln His Ala Leu Asp Phe Ser His Lys Thr  
 915 920 925  
 Ser Thr Lys Phe Asp Phe His Lys Glu Asn Phe  
 930 935

&lt;210&gt; 17

&lt;211&gt; 2532

&lt;212&gt; DNA

<213> *Oryza sativa*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(2529)

&lt;223&gt; coding for NADPH oxidase

&lt;400&gt; 17

atg gcg tcg ccg tac gac cac cag tcg ccg cat gcg cag cac ccg tcg	48
Met Ala Ser Pro Tyr Asp His Gln Ser Pro His Ala Gln His Pro Ser	
1 5 10 15	
ggg ttg ccg agg ccg ccg ggg gcg ggg gcg ggt gcg gcg gcg ggc ggg	96
Gly Leu Pro Arg Pro Pro Gly Ala Gly Ala Gly Ala Ala Ala Gly Gly	
20 25 30	
ttc gcg cgg ggg ctg atg aag cag ccg tcg cgg ctg gcg tcc ggg gtg	144
Phe Ala Arg Gly Leu Met Lys Gln Pro Ser Arg Leu Ala Ser Gly Val	
35 40 45	
agg cag ttc gcg tcg agg gtg tcg atg aag gtg ccg gag ggg gtg ggg	192
Arg Gln Phe Ala Ser Arg Val Ser Met Lys Val Pro Glu Gly Val Gly	
50 55 60	
ggg atg cgg ccc ggt ggc ggg agg atg acg cgg atg cag tcc agc gcg	240
Gly Met Arg Pro Gly Gly Gly Arg Met Thr Arg Met Gln Ser Ser Ala	
65 70 75 80	

cag	gtg	ggg	ctc	cgg	ggg	ctc	cgc	ttc	ctc	gac	aag	acg	tcc	ggc	ggg	288
Gln	Val	Gly	Leu	Arg	Gly	Leu	Arg	Phe	Leu	Asp	Lys	Thr	Ser	Gly	Gly	
			85						90					95		
aag	gag	ggg	tgg	aag	tcc	gtc	gag	cgc	cgc	ttc	gac	gag	atg	aac	cgc	336
Lys	Glu	Gly	Trp	Lys	Ser	Val	Glu	Arg	Arg	Phe	Asp	Glu	Met	Asn	Arg	
			100					105					110			
aac	ggc	cgc	ctc	ccc	aag	gag	agc	ttc	ggc	aag	tgc	atc	ggc	atg	ggg	384
Asn	Gly	Arg	Leu	Pro	Lys	Glu	Ser	Phe	Gly	Lys	Cys	Ile	Gly	Met	Gly	
		115					120					125				
gac	tcc	aag	gag	ttc	gcc	ggc	gag	ctg	ttc	gtg	gcg	ctg	gcg	cgg	cgg	432
Asp	Ser	Lys	Glu	Phe	Ala	Gly	Glu	Leu	Phe	Val	Ala	Leu	Ala	Arg	Arg	
	130					135					140					
agg	aac	ctg	gag	ccg	gag	gac	ggc	atc	acc	aag	gag	cag	ctc	aag	gag	480
Arg	Asn	Leu	Glu	Pro	Glu	Asp	Gly	Ile	Thr	Lys	Glu	Gln	Leu	Lys	Glu	
	145				150					155					160	
ttc	tgg	gag	gag	atg	acc	gac	cag	aac	ttc	gac	tcg	cgg	ctt	cgc	att	528
Phe	Trp	Glu	Glu	Met	Thr	Asp	Gln	Asn	Phe	Asp	Ser	Arg	Leu	Arg	Ile	
			165					170						175		
ttc	ttt	gac	atg	tgc	gac	aag	aat	ggc	gat	ggg	atg	ctc	acg	gaa	gat	576
Phe	Phe	Asp	Met	Cys	Asp	Lys	Asn	Gly	Asp	Gly	Met	Leu	Thr	Glu	Asp	
			180					185					190			
gag	gtc	aag	gag	gtt	att	ata	ctg	agt	gcg	tcg	gcg	aac	aag	ctg	gcg	624
Glu	Val	Lys	Glu	Val	Ile	Ile	Leu	Ser	Ala	Ser	Ala	Asn	Lys	Leu	Ala	
		195					200					205				
aag	ctg	aag	gga	cac	gcg	gcg	acg	tac	gcg	tcg	ctg	atc	atg	gag	gag	672
Lys	Leu	Lys	Gly	His	Ala	Ala	Thr	Tyr	Ala	Ser	Leu	Ile	Met	Glu	Glu	
	210					215					220					
ctg	gac	ccg	gac	gac	cgc	ggg	tac	atc	gag	atc	tgg	cag	ctg	gag	acg	720
Leu	Asp	Pro	Asp	Asp	Arg	Gly	Tyr	Ile	Glu	Ile	Trp	Gln	Leu	Glu	Thr	
	225				230					235				240		
ctg	ctg	cgc	ggc	atg	gtg	agc	gcg	cag	gcg	gcg	ccg	gag	aag	atg	aag	768
Leu	Leu	Arg	Gly	Met	Val	Ser	Ala	Gln	Ala	Ala	Pro	Glu	Lys	Met	Lys	
			245					250						255		
cgg	acg	acg	tcg	agc	ctc	gcg	agg	acg	atg	atc	ccg	tcg	cgg	tac	cgg	816
Arg	Thr	Thr	Ser	Ser	Leu	Ala	Arg	Thr	Met	Ile	Pro	Ser	Arg	Tyr	Arg	
			260					265					270			
agc	ccg	ctg	aag	cgg	cac	gtg	tcc	agg	acg	gtg	gac	ttc	gtg	cac	gag	864
Ser	Pro	Leu	Lys	Arg	His	Val	Ser	Arg	Thr	Val	Asp	Phe	Val	His	Glu	
		275					280					285				
aac	tgg	aag	cgg	atc	tgg	ctc	gtc	gcg	ctg	tgg	ctc	gcc	gtc	aac	gtc	912
Asn	Trp	Lys	Arg	Ile	Trp	Leu	Val	Ala	Leu	Trp	Leu	Ala	Val	Asn	Val	
	290					295					300					
ggc	ctc	ttc	gcc	tac	aag	ttc	gag	cag	tac	gag	cgg	cgc	gcc	gcg	ttc	960
Gly	Leu	Phe	Ala	Tyr	Lys	Phe	Glu	Gln	Tyr	Glu	Arg	Arg	Ala	Ala	Phe	
	305				310					315				320		
cag	gtg	atg	ggc	cac	tgc	gtg	tgc	gtg	gcc	aag	ggc	gcc	gcc	gag	gtg	1008
Gln	Val	Met	Gly	His	Cys	Val	Cys	Val	Ala	Lys	Gly	Ala	Ala	Glu	Val	
			325					330						335		
ctc	aag	ctc	aac	atg	gcg	ctc	atc	ctc	ctc	ccc	gtg	tgc	cgg	aac	acg	1056
Leu	Lys	Leu	Asn	Met	Ala	Leu	Ile	Leu	Leu	Pro	Val	Cys	Arg	Asn	Thr	
			340					345					350			
ctc	acc	acg	ctc	agg	tcc	acg	gcg	ctc	agc	cac	gtc	atc	ccc	ttc	gac	1104
Leu	Thr	Thr	Leu	Arg	Ser	Thr	Ala	Leu	Ser	His	Val	Ile	Pro	Phe	Asp	
		355					360					365				
gac	aac	atc	aac	ttc	cac	aag	gtg	atc	gcg	gcg	acc	atc	gcc	gcc	gcc	1152
Asp	Asn	Ile	Asn	Phe	His	Lys	Val	Ile	Ala	Ala	Thr	Ile	Ala	Ala	Ala	
	370					375					380					
acc	gcc	gtc	cac	acg	ctg	gcg	cac	gtc	acc	tgc	gac	ttc	ccg	agg	ctg	1200
Thr	Ala	Val	His	Thr	Leu	Ala	His	Val	Thr	Cys	Asp	Phe	Pro	Arg	Leu	
	385				390					395				400		
atc	aac	tgc	ccc	agc	gac	aag	ttc	atg	gcg	acg	ctg	ggg	ccg	aac	ttc	1248

Ile	Asn	Cys	Pro	Ser	Asp	Lys	Phe	Met	Ala	Thr	Leu	Gly	Pro	Asn	Phe	
				405					410					415		
ggg	tac	agg	cag	ccg	acg	tac	gcc	gac	ctg	ctg	gag	agc	gcc	ccc	ggc	1296
Gly	Tyr	Arg	Gln	Pro	Thr	Tyr	Ala	Asp	Leu	Leu	Glu	Ser	Ala	Pro	Gly	
			420					425					430			
gtc	acc	ggc	atc	ctc	atg	atc	atc	atg	tcc	ttc	tcc	ttc	acg	ctg		1344
Val	Thr	Gly	Ile	Leu	Met	Ile	Ile	Met	Ser	Phe	Ser	Phe	Thr	Leu		
			435				440					445				
gcc	acg	cac	tcc	ttc	cgc	cgg	agc	gtc	gtc	aag	ctg	ccg	tcg	ccg	ctg	1392
Ala	Thr	His	Ser	Phe	Arg	Arg	Ser	Val	Val	Lys	Leu	Pro	Ser	Pro	Leu	
			450				455				460					
cac	cac	ctc	gcc	ggc	ttc	aac	gcc	ttc	tgg	tac	gcg	cac	cac	ctc	ctg	1440
His	His	Leu	Ala	Gly	Phe	Asn	Ala	Phe	Trp	Tyr	Ala	His	His	Leu	Leu	
465					470					475					480	
gtg	ctc	gcc	tac	gtc	ctc	ctc	gtc	gtg	cac	tcc	tac	ttc	ata	ttc	ctc	1488
Val	Leu	Ala	Tyr	Val	Leu	Leu	Val	Val	His	Ser	Tyr	Phe	Ile	Phe	Leu	
				485					490					495		
acc	agg	gag	tgg	tac	aag	aaa	acg	aca	tgg	atg	tac	ctg	ata	gtc	cca	1536
Thr	Arg	Glu	Trp	Tyr	Lys	Lys	Thr	Thr	Trp	Met	Tyr	Leu	Ile	Val	Pro	
			500					505					510			
gtg	ctc	ttc	tat	gca	tgc	gag	aga	acg	atc	aga	aaa	gtt	cga	gag	aac	1584
Val	Leu	Phe	Tyr	Ala	Cys	Glu	Arg	Thr	Ile	Arg	Lys	Val	Arg	Glu	Asn	
			515				520					525				
aac	tac	cgc	gtg	agc	atc	gtc	aag	gca	gcg	att	tac	cca	gga	aat	gtg	1632
Asn	Tyr	Arg	Val	Ser	Ile	Val	Lys	Ala	Ala	Ile	Tyr	Pro	Gly	Asn	Val	
			530			535					540					
ctc	tct	ctt	cac	atg	aag	aag	ccg	ccg	ggt	ttc	aag	tac	aag	agc	ggg	1680
Leu	Ser	Leu	His	Met	Lys	Lys	Pro	Pro	Gly	Phe	Lys	Tyr	Lys	Ser	Gly	
545					550					555					560	
atg	tac	ctg	ttt	gtg	aag	tgc	cct	gat	gtc	tct	cct	ttc	gaa	tgg	cat	1728
Met	Tyr	Leu	Phe	Val	Lys	Cys	Pro	Asp	Val	Ser	Pro	Phe	Glu	Trp	His	
				565					570					575		
ccc	ttc	tcc	atc	act	tct	gca	cct	gga	gat	gac	tac	ctg	agt	gtg	cat	1776
Pro	Phe	Ser	Ile	Thr	Ser	Ala	Pro	Gly	Asp	Asp	Tyr	Leu	Ser	Val	His	
			580					585					590			
atc	cgt	aca	cta	ggt	gac	tgg	acg	act	gaa	ctc	aga	aac	ctg	ttt	ggg	1824
Ile	Arg	Thr	Leu	Gly	Asp	Trp	Thr	Thr	Glu	Leu	Arg	Asn	Leu	Phe	Gly	
			595				600					605				
aag	gct	tgc	gag	gca	cag	ggt	act	tct	aag	aag	gct	acc	ctt	tca	aga	1872
Lys	Ala	Cys	Glu	Ala	Gln	Val	Thr	Ser	Lys	Lys	Ala	Thr	Leu	Ser	Arg	
			610			615					620					
ctt	gaa	act	aca	ggt	gtg	gcg	gac	gct	cag	aca	gag	gat	act	agg	ttt	1920
Leu	Glu	Thr	Thr	Val	Val	Ala	Asp	Ala	Gln	Thr	Glu	Asp	Thr	Arg	Phe	
625				630					635						640	
cct	aag	gtc	ctt	att	gat	ggg	ccc	tat	ggt	gca	ccg	gcg	caa	aac	tac	1968
Pro	Lys	Val	Leu	Ile	Asp	Gly	Pro	Tyr	Gly	Ala	Pro	Ala	Gln	Asn	Tyr	
				645					650					655		
aag	aag	tat	gac	att	ctt	ttg	ctt	att	ggt	ctt	gga	att	ggt	gct	act	2016
Lys	Lys	Tyr	Asp	Ile	Leu	Leu	Leu	Ile	Gly	Leu	Gly	Ile	Gly	Ala	Thr	
			660					665					670			
cct	ttc	atc	agc	att	ctg	aag	gat	ctg	ttg	aac	aac	att	aaa	tcc	aac	2064
Pro	Phe	Ile	Ser	Ile	Leu	Lys	Asp	Leu	Leu	Asn	Asn	Ile	Lys	Ser	Asn	
			675				680					685				
gaa	gag	gtg	gaa	agc	ata	cat	ggt	tct	gag	ata	ggc	agc	ttc	aag	aac	2112
Glu	Glu	Val	Glu	Ser	Ile	His	Gly	Ser	Glu	Ile	Gly	Ser	Phe	Lys	Asn	
			690			695					700					
aat	ggg	cca	gga	aga	gct	tac	ttc	tac	tgg	gtg	acc	aga	gag	caa	ggg	2160
Asn	Gly	Pro	Gly	Arg	Ala	Tyr	Phe	Tyr	Trp	Val	Thr	Arg	Glu	Gln	Gly	
705				710					715						720	
tcc	ttc	gag	tgg	ttt	aaa	gga	gtc	atg	aac	gat	gtc	gct	gaa	agt	gat	2208
Ser	Phe	Glu	Trp	Phe	Lys	Gly	Val	Met	Asn	Asp	Val	Ala	Glu	Ser	Asp	



				725					730					735			
cac	aat	aat	att	ata	gag	atg	cac	aat	tac	ctg	acc	agc	gtg	tat	gaa		2256
His	Asn	Asn	Ile	Ile	Glu	Met	His	Asn	Tyr	Leu	Thr	Ser	Val	Tyr	Glu		
			740					745					750				
gaa	ggc	gac	gca	agg	tca	gct	ttg	att	gcc	atg	gtt	cag	tca	ctt	caa		2304
Glu	Gly	Asp	Ala	Arg	Ser	Ala	Leu	Ile	Ala	Met	Val	Gln	Ser	Leu	Gln		
		755					760					765					
cat	gcc	aaa	aat	ggg	gtg	gat	atc	gtc	tcc	ggc	agc	agg	att	cgc	aca		2352
His	Ala	Lys	Asn	Gly	Val	Asp	Ile	Val	Ser	Gly	Ser	Arg	Ile	Arg	Thr		
	770					775					780						
cat	ttt	gcg	agg	cct	aac	tgg	aga	aag	gtg	ttc	tct	gac	ttg	gcg	aat		2400
His	Phe	Ala	Arg	Pro	Asn	Trp	Arg	Lys	Val	Phe	Ser	Asp	Leu	Ala	Asn		
	785				790				795				800				
gcc	cac	aaa	aac	tca	cgc	ata	ggg	gtt	ttc	tat	tgt	gga	tcc	cct	aca		2448
Ala	His	Lys	Asn	Ser	Arg	Ile	Gly	Val	Phe	Tyr	Cys	Gly	Ser	Pro	Thr		
				805				810					815				
ctc	acg	aaa	caa	ctc	aag	gat	ctt	tca	aaa	gaa	ttc	agc	cag	aca	acc		2496
Leu	Thr	Lys	Gln	Leu	Lys	Asp	Leu	Ser	Lys	Glu	Phe	Ser	Gln	Thr	Thr		
		820					825					830					
aca	act	aga	ttc	cac	ttc	cac	aag	gaa	aac	ttt	taa						2532
Thr	Thr	Arg	Phe	His	Phe	His	Lys	Glu	Asn	Phe							
		835					840										

&lt;210&gt; 18

&lt;211&gt; 843

&lt;212&gt; PRT

&lt;213&gt; Oryza sativa

&lt;400&gt; 18

Met	Ala	Ser	Pro	Tyr	Asp	His	Gln	Ser	Pro	His	Ala	Gln	His	Pro	Ser		
1				5				10						15			
Gly	Leu	Pro	Arg	Pro	Pro	Gly	Ala	Gly	Ala	Gly	Ala	Ala	Ala	Gly	Gly		
			20					25					30				
Phe	Ala	Arg	Gly	Leu	Met	Lys	Gln	Pro	Ser	Arg	Leu	Ala	Ser	Gly	Val		
		35					40					45					
Arg	Gln	Phe	Ala	Ser	Arg	Val	Ser	Met	Lys	Val	Pro	Glu	Gly	Val	Gly		
	50					55					60						
Gly	Met	Arg	Pro	Gly	Gly	Gly	Arg	Met	Thr	Arg	Met	Gln	Ser	Ser	Ala		
	65				70				75						80		
Gln	Val	Gly	Leu	Arg	Gly	Leu	Arg	Phe	Leu	Asp	Lys	Thr	Ser	Gly	Gly		
				85				90						95			
Lys	Glu	Gly	Trp	Lys	Ser	Val	Glu	Arg	Arg	Phe	Asp	Glu	Met	Asn	Arg		
		100						105					110				
Asn	Gly	Arg	Leu	Pro	Lys	Glu	Ser	Phe	Gly	Lys	Cys	Ile	Gly	Met	Gly		
	115						120					125					
Asp	Ser	Lys	Glu	Phe	Ala	Gly	Glu	Leu	Phe	Val	Ala	Leu	Ala	Arg	Arg		
	130					135					140						
Arg	Asn	Leu	Glu	Pro	Glu	Asp	Gly	Ile	Thr	Lys	Glu	Gln	Leu	Lys	Glu		
	145				150				155						160		
Phe	Trp	Glu	Glu	Met	Thr	Asp	Gln	Asn	Phe	Asp	Ser	Arg	Leu	Arg	Ile		
				165					170						175		
Phe	Phe	Asp	Met	Cys	Asp	Lys	Asn	Gly	Asp	Gly	Met	Leu	Thr	Glu	Asp		
		180						185					190				
Glu	Val	Lys	Glu	Val	Ile	Ile	Leu	Ser	Ala	Ser	Ala	Asn	Lys	Leu	Ala		
	195						200					205					
Lys	Leu	Lys	Gly	His	Ala	Ala	Thr	Tyr	Ala	Ser	Leu	Ile	Met	Glu	Glu		
	210					215					220						
Leu	Asp	Pro	Asp	Asp	Arg	Gly	Tyr	Ile	Glu	Ile	Trp	Gln	Leu	Glu	Thr		
	225				230				235						240		
Leu	Leu	Arg	Gly	Met	Val	Ser	Ala	Gln	Ala	Ala	Pro	Glu	Lys	Met	Lys		
				245					250					255			

Arg	Thr	Thr	Ser	Ser	Leu	Ala	Arg	Thr	Met	Ile	Pro	Ser	Arg	Tyr	Arg		
			260					265					270				
Ser	Pro	Leu	Lys	Arg	His	Val	Ser	Arg	Thr	Val	Asp	Phe	Val	His	Glu		
		275					280					285					
Asn	Trp	Lys	Arg	Ile	Trp	Leu	Val	Ala	Leu	Trp	Leu	Ala	Val	Asn	Val		
	290					295					300						
Gly	Leu	Phe	Ala	Tyr	Lys	Phe	Glu	Gln	Tyr	Glu	Arg	Arg	Ala	Ala	Phe		
305					310					315					320		
Gln	Val	Met	Gly	His	Cys	Val	Cys	Val	Ala	Lys	Gly	Ala	Ala	Glu	Val		
				325					330					335			
Leu	Lys	Leu	Asn	Met	Ala	Leu	Ile	Leu	Leu	Pro	Val	Cys	Arg	Asn	Thr		
			340					345					350				
Leu	Thr	Thr	Leu	Arg	Ser	Thr	Ala	Leu	Ser	His	Val	Ile	Pro	Phe	Asp		
	355					360						365					
Asp	Asn	Ile	Asn	Phe	His	Lys	Val	Ile	Ala	Ala	Thr	Ile	Ala	Ala	Ala		
	370					375					380						
Thr	Ala	Val	His	Thr	Leu	Ala	His	Val	Thr	Cys	Asp	Phe	Pro	Arg	Leu		
385					390					395					400		
Ile	Asn	Cys	Pro	Ser	Asp	Lys	Phe	Met	Ala	Thr	Leu	Gly	Pro	Asn	Phe		
				405				410						415			
Gly	Tyr	Arg	Gln	Pro	Thr	Tyr	Ala	Asp	Leu	Leu	Glu	Ser	Ala	Pro	Gly		
			420					425					430				
Val	Thr	Gly	Ile	Leu	Met	Ile	Ile	Ile	Met	Ser	Phe	Ser	Phe	Thr	Leu		
	435					440						445					
Ala	Thr	His	Ser	Phe	Arg	Arg	Ser	Val	Val	Lys	Leu	Pro	Ser	Pro	Leu		
	450					455					460						
His	His	Leu	Ala	Gly	Phe	Asn	Ala	Phe	Trp	Tyr	Ala	His	His	Leu	Leu		
465					470					475					480		
Val	Leu	Ala	Tyr	Val	Leu	Leu	Val	Val	His	Ser	Tyr	Phe	Ile	Phe	Leu		
				485					490					495			
Thr	Arg	Glu	Trp	Tyr	Lys	Lys	Thr	Thr	Trp	Met	Tyr	Leu	Ile	Val	Pro		
			500					505					510				
Val	Leu	Phe	Tyr	Ala	Cys	Glu	Arg	Thr	Ile	Arg	Lys	Val	Arg	Glu	Asn		
	515						520					525					
Asn	Tyr	Arg	Val	Ser	Ile	Val	Lys	Ala	Ala	Ile	Tyr	Pro	Gly	Asn	Val		
	530					535					540						
Leu	Ser	Leu	His	Met	Lys	Lys	Pro	Pro	Gly	Phe	Lys	Tyr	Lys	Ser	Gly		
545					550					555					560		
Met	Tyr	Leu	Phe	Val	Lys	Cys	Pro	Asp	Val	Ser	Pro	Phe	Glu	Trp	His		
				565					570					575			
Pro	Phe	Ser	Ile	Thr	Ser	Ala	Pro	Gly	Asp	Asp	Tyr	Leu	Ser	Val	His		
			580					585					590				
Ile	Arg	Thr	Leu	Gly	Asp	Trp	Thr	Thr	Glu	Leu	Arg	Asn	Leu	Phe	Gly		
	595						600					605					
Lys	Ala	Cys	Glu	Ala	Gln	Val	Thr	Ser	Lys	Lys	Ala	Thr	Leu	Ser	Arg		
	610					615					620						
Leu	Glu	Thr	Thr	Val	Val	Ala	Asp	Ala	Gln	Thr	Glu	Asp	Thr	Arg	Phe		
625					630					635					640		
Pro	Lys	Val	Leu	Ile	Asp	Gly	Pro	Tyr	Gly	Ala	Pro	Ala	Gln	Asn	Tyr		
				645					650					655			
Lys	Lys	Tyr	Asp	Ile	Leu	Leu	Leu	Ile	Gly	Leu	Gly	Ile	Gly	Ala	Thr		
			660					665					670				
Pro	Phe	Ile	Ser	Ile	Leu	Lys	Asp	Leu	Leu	Asn	Asn	Ile	Lys	Ser	Asn		
	675						680					685					
Glu	Glu	Val	Glu	Ser	Ile	His	Gly	Ser	Glu	Ile	Gly	Ser	Phe	Lys	Asn		
	690					695					700						
Asn	Gly	Pro	Gly	Arg	Ala	Tyr	Phe	Tyr	Trp	Val	Thr	Arg	Glu	Gln	Gly		
705					710					715					720		
Ser	Phe	Glu	Trp	Phe	Lys	Gly	Val	Met	Asn	Asp	Val	Ala	Glu	Ser	Asp		
				725					730					735			
His	Asn	Asn	Ile	Ile	Glu	Met	His	Asn	Tyr	Leu	Thr	Ser	Val	Tyr	Glu		

740							745					750				
Glu	Gly	Asp	Ala	Arg	Ser	Ala	Leu	Ile	Ala	Met	Val	Gln	Ser	Leu	Gln	
755							760					765				
His	Ala	Lys	Asn	Gly	Val	Asp	Ile	Val	Ser	Gly	Ser	Arg	Ile	Arg	Thr	
770							775					780				
His	Phe	Ala	Arg	Pro	Asn	Trp	Arg	Lys	Val	Phe	Ser	Asp	Leu	Ala	Asn	
785							790					795				
Ala	His	Lys	Asn	Ser	Arg	Ile	Gly	Val	Phe	Tyr	Cys	Gly	Ser	Pro	Thr	
805							810					815				
Leu	Thr	Lys	Gln	Leu	Lys	Asp	Leu	Ser	Lys	Glu	Phe	Ser	Gln	Thr	Thr	
820							825					830				
Thr	Thr	Arg	Phe	His	Phe	His	Lys	Glu	Asn	Phe						
835							840									

```
<210> 19
<211> 2604
<212> DNA
<213> Arabidopsis thaliana
```

```
<220>  
<221> CDS  
<222> (1)..(2601)  
<223> coding for NADPH oxidase
```

<400> 19																
atg	tct	aga	gtg	agt	ttt	gaa	gtg	tca	gga	ggc	tat	cac	tct	gat	gca	48
Met	Ser	Arg	Val	Ser	Phe	Glu	Val	Ser	Gly	Gly	Tyr	His	Ser	Asp	Ala	
1				5					10					15		
gaa	gcc	gga	aac	agc	gga	cca	atg	agc	ggg	ggg	caa	tta	cca	ccg	atc	96
Glu	Ala	Gly	Asn	Ser	Gly	Pro	Met	Ser	Gly	Gly	Gln	Leu	Pro	Pro	Ile	
			20					25					30			
tat	aaa	aaa	ccg	ggg	aac	tcc	aga	ttc	act	gct	gag	aac	agt	cag	aga	144
Tyr	Lys	Lys	Pro	Gly	Asn	Ser	Arg	Phe	Thr	Ala	Glu	Asn	Ser	Gln	Arg	
		35					40					45				
aca	cgt	acg	gca	cca	tac	gtg	gac	ctc	acg	gta	gat	gta	caa	gac	gat	192
Thr	Arg	Thr	Ala	Pro	Tyr	Val	Asp	Leu	Thr	Val	Asp	Val	Gln	Asp	Asp	
	50					55					60					
aca	gtc	tct	gta	cat	agc	ttg	aaa	atg	gaa	ggg	gga	tct	agc	gtt	gaa	240
Thr	Val	Ser	Val	His	Ser	Leu	Lys	Met	Glu	Gly	Gly	Ser	Ser	Val	Glu	
65					70					75				80		
gag	agt	ccg	gag	ctt	act	ttg	ctg	aaa	cga	aac	cgt	ctt	gag	aag	aaa	288
Glu	Ser	Pro	Glu	Leu	Thr	Leu	Leu	Lys	Arg	Asn	Arg	Leu	Glu	Lys	Lys	
				85					90					95		
aca	acg	gtg	gtg	aaa	cgt	ttg	gcg	tct	gtt	tct	cac	gag	ctt	aag	cgt	336
Thr	Thr	Val	Val	Lys	Arg	Leu	Ala	Ser	Val	Ser	His	Glu	Leu	Lys	Arg	
		100						105					110			
ttg	aca	tct	gtt	tct	ggg	ggg	att	ggg	gga	aga	aag	ccg	cct	cga	ccg	384
Leu	Thr	Ser	Val	Ser	Gly	Gly	Ile	Gly	Gly	Arg	Lys	Pro	Pro	Arg	Pro	
		115					120					125				
gct	aag	tta	gac	cgg	act	aaa	tcc	gcc	gcg	agt	caa	gcg	ttg	aag	gga	432
Ala	Lys	Leu	Asp	Arg	Thr	Lys	Ser	Ala	Ala	Ser	Gln	Ala	Leu	Lys	Gly	
	130					135					140					
ctt	aag	ttc	att	agt	aaa	acc	gac	ggg	ggc	gcc	ggg	tgg	tct	gcc	gtg	480
Leu	Lys	Phe	Ile	Ser	Lys	Thr	Asp	Gly	Gly	Ala	Gly	Trp	Ser	Ala	Val	
145					150					155				160		
gag	aag	cgg	ttt	aat	cag	att	acc	gcg	act	acc	ggg	gga	cta	ctt	ctt	528
Glu	Lys	Arg	Phe	Asn	Gln	Ile	Thr	Ala	Thr	Thr	Gly	Gly	Leu	Leu	Leu	
				165					170					175		
cgg	aca	aag	ttc	ggg	gaa	tgc	ata	gga	atg	act	tca	aag	gat	ttt	gct	576
Arg	Thr	Lys	Phe	Gly	Glu	Cys	Ile	Gly	Met	Thr	Ser	Lys	Asp	Phe	Ala	
			180					185					190			

ttg	gaa	ctg	ttt	gat	gca	ttg	gct	aga	aga	agg	aat	ata	aca	ggg	gaa	624
Leu	Glu	Leu	Phe	Asp	Ala	Leu	Ala	Arg	Arg	Arg	Asn	Ile	Thr	Gly	Glu	
	195						200					205				
gtg	att	gat	gga	gat	caa	cta	aag	gag	ttt	tgg	gaa	caa	att	aat	gat	672
Val	Ile	Asp	Gly	Asp	Gln	Leu	Lys	Glu	Phe	Trp	Glu	Gln	Ile	Asn	Asp	
	210						215				220					
caa	agt	ttt	gat	tct	cgg	ctt	aag	aca	ttc	ttt	gac	atg	gtg	gat	aaa	720
Gln	Ser	Phe	Asp	Ser	Arg	Leu	Lys	Thr	Phe	Phe	Asp	Met	Val	Asp	Lys	
225					230					235					240	
gat	gct	gat	ggg	aga	ctt	aca	gaa	gac	gaa	gtt	aga	gag	ttg	gag	agt	768
Asp	Ala	Asp	Gly	Arg	Leu	Thr	Glu	Asp	Glu	Val	Arg	Glu	Leu	Glu	Ser	
				245				250						255		
ctt	gag	act	ctg	ctt	ttg	caa	gcg	gca	aca	cag	tct	gtg	ata	aca	agt	816
Leu	Glu	Thr	Leu	Leu	Leu	Gln	Ala	Ala	Thr	Gln	Ser	Val	Ile	Thr	Ser	
			260					265					270			
act	ggg	gag	aga	aag	aat	ctg	agt	cat	atg	atg	agt	cag	agg	ctt	aag	864
Thr	Gly	Glu	Arg	Lys	Asn	Leu	Ser	His	Met	Met	Ser	Gln	Arg	Leu	Lys	
	275						280					285				
cct	acg	ttt	aac	cgc	aac	ccg	ttg	aag	cga	tgg	tac	cgt	ggg	ctt	aga	912
Pro	Thr	Phe	Asn	Arg	Asn	Pro	Leu	Lys	Arg	Trp	Tyr	Arg	Gly	Leu	Arg	
	290					295					300					
ttc	ttc	ttg	tta	gac	aac	tgg	caa	aga	tgt	tgg	gtt	ata	gtg	cta	tgg	960
Phe	Phe	Leu	Leu	Asp	Asn	Trp	Gln	Arg	Cys	Trp	Val	Ile	Val	Leu	Trp	
305					310					315					320	
ttc	ata	gtt	atg	gct	ata	ctc	ttc	acc	tac	aaa	tat	atc	caa	tac	agg	1008
Phe	Ile	Val	Met	Ala	Ile	Leu	Phe	Thr	Tyr	Lys	Tyr	Ile	Gln	Tyr	Arg	
				325					330					335		
cgt	agc	cct	gtg	tat	cca	gtg	atg	ggg	gat	tgt	gtg	tgc	atg	gct	aaa	1056
Arg	Ser	Pro	Val	Tyr	Pro	Val	Met	Gly	Asp	Cys	Val	Cys	Met	Ala	Lys	
			340					345				350				
ggg	gct	gca	gaa	aca	gtg	aag	ctg	aac	atg	gct	ttg	att	ctc	tta	cct	1104
Gly	Ala	Ala	Glu	Thr	Val	Lys	Leu	Asn	Met	Ala	Leu	Ile	Leu	Leu	Pro	
	355						360					365				
gtt	tgt	aga	aac	acc	atc	aca	tgg	ctt	aga	aat	aag	acc	agg	ttg	ggg	1152
Val	Cys	Arg	Asn	Thr	Ile	Thr	Trp	Leu	Arg	Asn	Lys	Thr	Arg	Leu	Gly	
	370					375					380					
cgt	gtt	gtc	cca	ttt	gat	gac	aat	ctc	aac	ttc	cac	aag	gtt	ata	gcg	1200
Arg	Val	Val	Pro	Phe	Asp	Asp	Asn	Leu	Asn	Phe	His	Lys	Val	Ile	Ala	
385					390					395					400	
gtg	ggg	att	ata	gtt	gga	gta	acg	atg	cac	gcc	ggg	gca	cat	tta	gcg	1248
Val	Gly	Ile	Ile	Val	Gly	Val	Thr	Met	His	Ala	Gly	Ala	His	Leu	Ala	
				405					410					415		
tgt	gat	ttc	ccg	cgg	tta	cta	cat	gca	act	cca	gag	gca	tat	agg	cct	1296
Cys	Asp	Phe	Pro	Arg	Leu	Leu	His	Ala	Thr	Pro	Glu	Ala	Tyr	Arg	Pro	
			420					425					430			
tta	aga	cag	ttt	ttt	ggg	gat	gag	caa	cca	aag	agc	tac	tgg	cat	ttt	1344
Leu	Arg	Gln	Phe	Phe	Gly	Asp	Glu	Gln	Pro	Lys	Ser	Tyr	Trp	His	Phe	
	435						440						445			
gta	aac	tcg	gta	gaa	ggg	ata	acc	gga	ctt	gtg	atg	gtt	ttg	tta	atg	1392
Val	Asn	Ser	Val	Glu	Gly	Ile	Thr	Gly	Leu	Val	Met	Val	Leu	Leu	Met	
	450					455					460					
gcg	att	gca	ttc	aca	cta	gcc	acg	cct	tgg	ttc	aga	aga	ggg	aag	cta	1440
Ala	Ile	Ala	Phe	Thr	Leu	Ala	Thr	Pro	Trp	Phe	Arg	Arg	Gly	Lys	Leu	
465					470					475					480	
aac	tat	ctt	cca	gga	cca	tta	aag	aaa	cta	gct	agc	ttc	aat	gcc	ttc	1488
Asn	Tyr	Leu	Pro	Gly	Pro	Leu	Lys	Lys	Leu	Ala	Ser	Phe	Asn	Ala	Phe	
				485					490					495		
tgg	tac	act	cat	cat	ttg	ttt	gtc	ata	gtc	tac	att	ctt	ctt	gtt	gct	1536
Trp	Tyr	Thr	His	His	Leu	Phe	Val	Ile	Val	Tyr	Ile	Leu	Leu	Val	Ala	
			500					505					510			
cat	gga	tac	tac	ttg	tat	ctc	acc	aga	gac	tgg	cac	aat	aaa	acg	act	1584

His	Gly	Tyr	Tyr	Leu	Tyr	Leu	Thr	Arg	Asp	Trp	His	Asn	Lys	Thr	Thr	
		515					520					525				
tgg	atg	tat	ttg	gtg	gta	cca	gtg	gtt	cta	tac	gcg	tgt	gaa	agg	ttg	1632
Trp	Met	Tyr	Leu	Val	Val	Pro	Val	Val	Leu	Tyr	Ala	Cys	Glu	Arg	Leu	
	530					535					540					
ata	aga	gca	ttc	agg	tcg	agc	atc	aag	gcg	gtg	act	att	agg	aaa	gta	1680
Ile	Arg	Ala	Phe	Arg	Ser	Ser	Ile	Lys	Ala	Val	Thr	Ile	Arg	Lys	Val	
545					550				555						560	
gca	gtt	tat	cca	gga	aac	gtg	ctg	gca	att	cac	ttg	tca	agg	cct	caa	1728
Ala	Val	Tyr	Pro	Gly	Asn	Val	Leu	Ala	Ile	His	Leu	Ser	Arg	Pro	Gln	
			565					570						575		
aac	ttc	aaa	tac	aag	agt	ggt	caa	tac	atg	ttt	gtt	aac	tgt	gct	gct	1776
Asn	Phe	Lys	Tyr	Lys	Ser	Gly	Gln	Tyr	Met	Phe	Val	Asn	Cys	Ala	Ala	
		580						585					590			
gtt	tct	cca	ttt	gaa	tgg	cat	cca	ttt	tca	atc	aca	tct	gca	cca	caa	1824
Val	Ser	Pro	Phe	Glu	Trp	His	Pro	Phe	Ser	Ile	Thr	Ser	Ala	Pro	Gln	
		595				600						605				
gat	gat	tac	cta	agt	gtt	cac	att	aga	gtt	ctt	ggg	gat	tgg	aca	cga	1872
Asp	Asp	Tyr	Leu	Ser	Val	His	Ile	Arg	Val	Leu	Gly	Asp	Trp	Thr	Arg	
	610					615					620					
gct	ctc	aaa	gga	gtc	ttc	tct	gag	gtg	tgt	aag	cca	cca	ccg	gca	gga	1920
Ala	Leu	Lys	Gly	Val	Phe	Ser	Glu	Val	Cys	Lys	Pro	Pro	Pro	Ala	Gly	
625					630				635						640	
gtt	agt	ggt	ctg	ctt	aga	gcc	gac	atg	ttg	cat	ggt	gca	aat	aat	ccc	1968
Val	Ser	Gly	Leu	Arg	Ala	Asp	Met	Leu	His	Gly	Ala	Asn	Asn	Pro		
			645					650					655			
gac	ttc	ccg	aaa	gtc	ttg	att	gat	ggt	cca	tat	ggt	gca	cca	gca	caa	2016
Asp	Phe	Pro	Lys	Val	Leu	Ile	Asp	Gly	Pro	Tyr	Gly	Ala	Pro	Ala	Gln	
		660						665					670			
gac	tac	aag	aag	tac	gag	gtg	gtt	cta	cta	gtt	ggt	ctc	ggg	att	gga	2064
Asp	Tyr	Lys	Lys	Tyr	Glu	Val	Val	Leu	Leu	Val	Gly	Leu	Gly	Ile	Gly	
		675						680					685			
gcc	aca	cca	atg	atc	agt	atc	gtc	aaa	gac	att	gtt	aat	aac	atc	aag	2112
Ala	Thr	Pro	Met	Ile	Ser	Ile	Val	Lys	Asp	Ile	Val	Asn	Asn	Ile	Lys	
	690					695					700					
gcc	aag	gaa	caa	gcc	caa	cta	aac	cga	atg	gag	aat	gga	aca	agc	gaa	2160
Ala	Lys	Glu	Gln	Ala	Gln	Leu	Asn	Arg	Met	Glu	Asn	Gly	Thr	Ser	Glu	
705					710				715						720	
cca	caa	cga	agt	aag	aaa	gag	agt	ttc	agg	acc	cgt	aga	gct	tac	ttc	2208
Pro	Gln	Arg	Ser	Lys	Lys	Glu	Ser	Phe	Arg	Thr	Arg	Arg	Ala	Tyr	Phe	
			725					730						735		
tat	tgg	gtt	acg	cgt	gag	caa	ggc	tct	ttc	gat	tgg	ttc	aag	aac	ata	2256
Tyr	Trp	Val	Thr	Arg	Glu	Gln	Gly	Ser	Phe	Asp	Trp	Phe	Lys	Asn	Ile	
		740						745					750			
atg	aac	gaa	gtc	gcg	gaa	cga	gat	gcc	aac	cgc	gtc	atc	gaa	atg	cat	2304
Met	Asn	Glu	Val	Ala	Glu	Arg	Asp	Ala	Asn	Arg	Val	Ile	Glu	Met	His	
		755					760					765				
aac	tat	tgt	aca	agt	gtc	tat	gaa	gaa	ggt	gac	gct	cgt	tcc	gca	ctt	2352
Asn	Tyr	Cys	Thr	Ser	Val	Tyr	Glu	Glu	Gly	Asp	Ala	Arg	Ser	Ala	Leu	
		770				775					780					
ata	cat	atg	ctt	caa	tca	cta	aac	cat	gca	aag	aac	ggc	gtc	gac	att	2400
Ile	His	Met	Leu	Gln	Ser	Leu	Asn	His	Ala	Lys	Asn	Gly	Val	Asp	Ile	
785					790				795						800	
gtc	tct	gga	aca	aga	gtt	atg	tcc	cat	ttc	gct	aaa	cct	aat	tgg	aga	2448
Val	Ser	Gly	Thr	Arg	Val	Met	Ser	His	Phe	Ala	Lys	Pro	Asn	Trp	Arg	
			805					810						815		
aat	gtt	tac	aag	cgt	ata	gct	atg	gat	cat	cct	aac	acc	aaa	gtt	gga	2496
Asn	Val	Tyr	Lys	Arg	Ile	Ala	Met	Asp	His	Pro	Asn	Thr	Lys	Val	Gly	
		820						825					830			
gtg	ttt	tac	tgt	gga	gca	cca	gca	ttg	aca	aag	gag	cta	agg	cat	cta	2544
Val	Phe	Tyr	Cys	Gly	Ala	Pro	Ala	Leu	Thr	Lys	Glu	Leu	Arg	His	Leu	

835	840	845	
gct tta gat ttc acc cac aaa aca agc acc aga ttc tcc ttc cac aaa			2592
Ala Leu Asp Phe Thr His Lys Thr Ser Thr Arg Phe Ser Phe His Lys			
850	855	860	
gag aat ttc taa			2604
Glu Asn Phe			
865			

<210> 20  
 <211> 867  
 <212> PRT  
 <213> Arabidopsis thaliana

<400> 20

Met	Ser	Arg	Val	Ser	Phe	Glu	Val	Ser	Gly	Gly	Tyr	His	Ser	Asp	Ala
1				5					10					15	
Glu	Ala	Gly	Asn	Ser	Gly	Pro	Met	Ser	Gly	Gly	Gln	Leu	Pro	Pro	Ile
			20					25					30		
Tyr	Lys	Lys	Pro	Gly	Asn	Ser	Arg	Phe	Thr	Ala	Glu	Asn	Ser	Gln	Arg
		35					40					45			
Thr	Arg	Thr	Ala	Pro	Tyr	Val	Asp	Leu	Thr	Val	Asp	Val	Gln	Asp	Asp
		50				55					60				
Thr	Val	Ser	Val	His	Ser	Leu	Lys	Met	Glu	Gly	Gly	Ser	Ser	Val	Glu
65					70					75					80
Glu	Ser	Pro	Glu	Leu	Thr	Leu	Leu	Lys	Arg	Asn	Arg	Leu	Glu	Lys	Lys
				85					90					95	
Thr	Thr	Val	Val	Lys	Arg	Leu	Ala	Ser	Val	Ser	His	Glu	Leu	Lys	Arg
			100					105					110		
Leu	Thr	Ser	Val	Ser	Gly	Gly	Ile	Gly	Gly	Arg	Lys	Pro	Pro	Arg	Pro
			115				120					125			
Ala	Lys	Leu	Asp	Arg	Thr	Lys	Ser	Ala	Ala	Ser	Gln	Ala	Leu	Lys	Gly
						135					140				
Leu	Lys	Phe	Ile	Ser	Lys	Thr	Asp	Gly	Gly	Ala	Gly	Trp	Ser	Ala	Val
145					150					155					160
Glu	Lys	Arg	Phe	Asn	Gln	Ile	Thr	Ala	Thr	Gly	Gly	Leu	Leu	Leu	
				165					170				175		
Arg	Thr	Lys	Phe	Gly	Glu	Cys	Ile	Gly	Met	Thr	Ser	Lys	Asp	Phe	Ala
			180					185					190		
Leu	Glu	Leu	Phe	Asp	Ala	Leu	Ala	Arg	Arg	Arg	Asn	Ile	Thr	Gly	Glu
							200					205			
Val	Ile	Asp	Gly	Asp	Gln	Leu	Lys	Glu	Phe	Trp	Glu	Gln	Ile	Asn	Asp
						215					220				
Gln	Ser	Phe	Asp	Ser	Arg	Leu	Lys	Thr	Phe	Phe	Asp	Met	Val	Asp	Lys
225					230					235					240
Asp	Ala	Asp	Gly	Arg	Leu	Thr	Glu	Asp	Glu	Val	Arg	Glu	Leu	Glu	Ser
				245					250					255	
Leu	Glu	Thr	Leu	Leu	Leu	Gln	Ala	Ala	Thr	Gln	Ser	Val	Ile	Thr	Ser
			260					265					270		
Thr	Gly	Glu	Arg	Lys	Asn	Leu	Ser	His	Met	Met	Ser	Gln	Arg	Leu	Lys
			275					280					285		
Pro	Thr	Phe	Asn	Arg	Asn	Pro	Leu	Lys	Arg	Trp	Tyr	Arg	Gly	Leu	Arg
						295					300				
Phe	Phe	Leu	Leu	Asp	Asn	Trp	Gln	Arg	Cys	Trp	Val	Ile	Val	Leu	Trp
305					310					315					320
Phe	Ile	Val	Met	Ala	Ile	Leu	Phe	Thr	Tyr	Lys	Tyr	Ile	Gln	Tyr	Arg
				325					330					335	
Arg	Ser	Pro	Val	Tyr	Pro	Val	Met	Gly	Asp	Cys	Val	Cys	Met	Ala	Lys
			340					345					350		
Gly	Ala	Ala	Glu	Thr	Val	Lys	Leu	Asn	Met	Ala	Leu	Ile	Leu	Leu	Pro
			355				360					365			
Val	Cys	Arg	Asn	Thr	Ile	Thr	Trp	Leu	Arg	Asn	Lys	Thr	Arg	Leu	Gly

370	375	380
Arg Val Val Pro Phe Asp	Asp Asn Leu Asn Phe	His Lys Val Ile Ala
385	390	395
Val Gly Ile Ile Val Gly	Val Thr Met His Ala Gly	Ala His Leu Ala
405	410	415
Cys Asp Phe Pro Arg Leu Leu	His Ala Thr Pro Glu Ala Tyr Arg Pro	
420	425	430
Leu Arg Gln Phe Phe Gly Asp	Glu Gln Pro Lys Ser Tyr Trp His Phe	
435	440	445
Val Asn Ser Val Glu Gly Ile Thr Gly	Leu Val Met Val Leu Leu Met	
450	455	460
Ala Ile Ala Phe Thr Leu Ala Thr	Pro Trp Phe Arg Arg Gly Lys Leu	
465	470	475
Asn Tyr Leu Pro Gly Pro Leu Lys	Lys Leu Ala Ser Phe Asn Ala Phe	
485	490	495
Trp Tyr Thr His His Leu Phe Val	Ile Val Tyr Ile Leu Leu Val Ala	
500	505	510
His Gly Tyr Tyr Leu Tyr Leu Thr	Arg Asp Trp His Asn Lys Thr Thr	
515	520	525
Trp Met Tyr Leu Val Val Pro Val	Val Leu Tyr Ala Cys Glu Arg Leu	
530	535	540
Ile Arg Ala Phe Arg Ser Ser Ile	Lys Ala Val Thr Ile Arg Lys Val	
545	550	555
Ala Val Tyr Pro Gly Asn Val Leu	Ala Ile His Leu Ser Arg Pro Gln	
565	570	575
Asn Phe Lys Tyr Lys Ser Gly Gln	Tyr Met Phe Val Asn Cys Ala Ala	
580	585	590
Val Ser Pro Phe Glu Trp His Pro	Phe Ser Ile Thr Ser Ala Pro Gln	
595	600	605
Asp Asp Tyr Leu Ser Val His Ile	Arg Val Leu Gly Asp Trp Thr Arg	
610	615	620
Ala Leu Lys Gly Val Phe Ser Glu	Val Cys Lys Pro Pro Pro Ala Gly	
625	630	635
Val Ser Gly Leu Leu Arg Ala Asp	Met Leu His Gly Ala Asn Asn Pro	
645	650	655
Asp Phe Pro Lys Val Leu Ile Asp	Gly Pro Tyr Gly Ala Pro Ala Gln	
660	665	670
Asp Tyr Lys Lys Tyr Glu Val Val	Leu Leu Val Gly Leu Gly Ile Gly	
675	680	685
Ala Thr Pro Met Ile Ser Ile Val	Lys Asp Ile Val Asn Asn Ile Lys	
690	695	700
Ala Lys Glu Gln Ala Gln Leu Asn	Arg Met Glu Asn Gly Thr Ser Glu	
705	710	715
Pro Gln Arg Ser Lys Glu Ser Phe	Arg Thr Arg Arg Ala Tyr Phe	
725	730	735
Tyr Trp Val Thr Arg Glu Gln Gly	Ser Phe Asp Trp Phe Lys Asn Ile	
740	745	750
Met Asn Glu Val Ala Glu Arg Asp	Ala Asn Arg Val Ile Glu Met His	
755	760	765
Asn Tyr Cys Thr Ser Val Tyr Glu	Glu Gly Asp Ala Arg Ser Ala Leu	
770	775	780
Ile His Met Leu Gln Ser Leu Asn	His Ala Lys Asn Gly Val Asp Ile	
785	790	795
Val Ser Gly Thr Arg Val Met Ser	His Phe Ala Lys Pro Asn Trp Arg	
805	810	815
Asn Val Tyr Lys Arg Ile Ala Met	Asp His Pro Asn Thr Lys Val Gly	
820	825	830
Val Phe Tyr Cys Gly Ala Pro Ala	Leu Thr Lys Glu Leu Arg His Leu	
835	840	845
Ala Leu Asp Phe Thr His Lys Thr	Ser Thr Arg Phe Ser Phe His Lys	
850	855	860

Glu Asn Phe  
865

<210> 21

<211> 2709

<212> DNA

<213> *Arabidopsis thaliana*

<220>

<221> CDS

<222> (1)..(2706)

<223> coding for NADPH oxidase

<400> 21

atg atg aat cga agt gaa atg caa aag tta ggt ttc gaa cac gtg aga	48
Met Met Asn Arg Ser Glu Met Gln Lys Leu Gly Phe Glu His Val Arg	
1 5 10 15	
tac tac aca gag tcg ccg tac aac aga gga gag tcc tcg gcg aac gtg	96
Tyr Tyr Thr Glu Ser Pro Tyr Asn Arg Gly Glu Ser Ser Ala Asn Val	
20 25 30	
gcg acg aca agc aac tat tac ggt gaa gat gaa cca tac gtg gag atc	144
Ala Thr Thr Ser Asn Tyr Tyr Gly Glu Asp Glu Pro Tyr Val Glu Ile	
35 40 45	
acg cta gat atc cac gac gat tcc gtc tcc gtg tac ggc ttg aag tca	192
Thr Leu Asp Ile His Asp Asp Ser Val Ser Val Tyr Gly Leu Lys Ser	
50 55 60	
ccg aac cat cga ggg gcc ggg tct aat tat gag gat caa tcg ctt ctc	240
Pro Asn His Arg Gly Ala Gly Ser Asn Tyr Glu Asp Gln Ser Leu Leu	
65 70 75 80	
aga caa ggt cgt tca ggg agg agt aac tcg gta ttg aaa cgc ttg gct	288
Arg Gln Gly Arg Ser Gly Arg Ser Asn Ser Val Leu Lys Arg Leu Ala	
85 90 95	
tct tct gtt tcc acc gga ata aca cga gtt gct tct tct gtt tct tcg	336
Ser Ser Val Ser Thr Gly Ile Thr Arg Val Ala Ser Ser Val Ser Ser	
100 105 110	
tct tcc gcg aga aaa cca ccg ccg cag ctg gct aag ctg cgc cgt	384
Ser Ser Ala Arg Lys Pro Pro Arg Pro Gln Leu Ala Lys Leu Arg Arg	
115 120 125	
tcg aaa tct aga gca gag cta gct ctc aaa ggt ctt aaa ttc atc acc	432
Ser Lys Ser Arg Ala Glu Leu Ala Leu Lys Gly Leu Lys Phe Ile Thr	
130 135 140	
aag act gat ggt gtc act ggt tgg cct gaa gtt gag aaa cgg ttt tat	480
Lys Thr Asp Gly Val Thr Gly Trp Pro Glu Val Glu Lys Arg Phe Tyr	
145 150 155 160	
gtg atg aca atg act aat aac gga tta tta cac cga tcc aga ttc ggt	528
Val Met Thr Met Thr Asn Asn Gly Leu Leu His Arg Ser Arg Phe Gly	
165 170 175	
gaa tgt ata ggg atg aaa tcg acg gag ttt gcg ttg gca ttg ttc gat	576
Glu Cys Ile Gly Met Lys Ser Thr Glu Phe Ala Leu Ala Leu Phe Asp	
180 185 190	
gct tta gcg agg agg gaa aac gta agc gga gat tca ata aac atg aat	624
Ala Leu Ala Arg Arg Glu Asn Val Ser Gly Asp Ser Ile Asn Met Asn	
195 200 205	
gag ctt aaa gag ttc tgg aag cag atc act gat caa gat ttt gat tca	672
Glu Leu Lys Glu Phe Trp Lys Gln Ile Thr Asp Gln Asp Phe Asp Ser	
210 215 220	
agg cta cga act ttc ttc gcc atg gtc gat aag gat tcg gat ggg ccg	720
Arg Leu Arg Thr Phe Phe Ala Met Val Asp Lys Asp Ser Asp Gly Arg	
225 230 235 240	
ttg aat gaa gcc gaa gta aga gag att ata act tta agt gct tct gca	768
Leu Asn Glu Ala Glu Val Arg Glu Ile Ile Thr Leu Ser Ala Ser Ala	



				245				250				255					
aac	gag	ttg	gat	aac	att	cgg	aga	caa	gct	gat	gaa	tat	gct	gct	ttg	816	
Asn	Glu	Leu	Asp	Asn	Ile	Arg	Arg	Gln	Ala	Asp	Glu	Tyr	Ala	Ala	Leu		
260				265				270									
att	atg	gaa	gaa	ctc	gat	cct	tat	cat	tat	gga	tac	atc	atg	ata	gag	864	
Ile	Met	Glu	Glu	Leu	Asp	Pro	Tyr	His	Tyr	Gly	Tyr	Ile	Met	Ile	Glu		
275				280				285									
aat	ctc	gag	ata	ctt	cta	ttg	caa	gcg	ccg	atg	cag	gat	gtg	aga	gat	912	
Asn	Leu	Glu	Ile	Leu	Leu	Leu	Gln	Ala	Pro	Met	Gln	Asp	Val	Arg	Asp		
290				295				300									
gga	gag	agt	aag	aag	cta	agc	aag	atg	cta	agt	cag	aat	ctc	atg	gtt	960	
Gly	Glu	Ser	Lys	Lys	Leu	Ser	Lys	Met	Leu	Ser	Gln	Asn	Leu	Met	Val		
305				310				315				320					
ccg	cag	agt	agg	aat	ctc	ggg	gca	cgt	ttt	tgc	aga	ggg	atg	aag	tat	1008	
Pro	Gln	Ser	Arg	Asn	Leu	Gly	Ala	Arg	Phe	Cys	Arg	Gly	Met	Lys	Tyr		
325				330				335									
ttt	ttg	ttt	gat	aat	tg	aag	aga	gtg	tg	gtg	atg	gct	cta	tg	ata	1056	
Phe	Leu	Phe	Asp	Asn	Trp	Lys	Arg	Val	Trp	Val	Met	Ala	Leu	Trp	Ile		
340				345				350									
ggt	gct	atg	gcg	ggt	ttg	ttc	acg	tg	aag	ttt	atg	gag	tat	cga	aaa	1104	
Gly	Ala	Met	Ala	Gly	Leu	Phe	Thr	Trp	Lys	Phe	Met	Glu	Tyr	Arg	Lys		
355				360				365									
aga	tcc	gct	tac	gaa	gtc	atg	gga	gtt	tgt	gtt	tgt	ata	gct	aaa	gga	1152	
Arg	Ser	Ala	Tyr	Glu	Val	Met	Gly	Val	Cys	Val	Cys	Ile	Ala	Lys	Gly		
370				375				380									
gct	gca	gag	acg	ctt	aaa	cta	aac	atg	gct	atg	att	ttg	tta	cca	gtt	1200	
Ala	Ala	Glu	Thr	Leu	Lys	Leu	Asn	Met	Ala	Met	Ile	Leu	Leu	Pro	Val		
385				390				395				400					
tgt	agg	aac	acc	atc	act	tg	ctg	cgg	acc	aaa	acc	aag	tta	agt	gct	1248	
Cys	Arg	Asn	Thr	Ile	Thr	Trp	Leu	Arg	Thr	Lys	Thr	Lys	Leu	Ser	Ala		
405				410				415									
att	gtt	cct	ttc	gat	gac	agc	ctc	aat	ttt	cac	aag	gtc	ata	gct	ata	1296	
Ile	Val	Pro	Phe	Asp	Asp	Ser	Leu	Asn	Phe	His	Lys	Val	Ile	Ala	Ile		
420				425				430									
gga	att	tca	gtt	gga	gtt	gga	atc	cat	gct	aca	tct	cac	tta	gca	tgt	1344	
Gly	Ile	Ser	Val	Gly	Val	Gly	Ile	His	Ala	Thr	Ser	His	Leu	Ala	Cys		
435				440				445									
gat	ttc	ccc	cga	ctg	ata	gct	gca	gac	gaa	gat	cag	tat	gag	cca	atg	1392	
Asp	Phe	Pro	Arg	Leu	Ile	Ala	Ala	Asp	Glu	Asp	Gln	Tyr	Glu	Pro	Met		
450				455				460									
gag	aag	tat	ttt	ggg	cca	cag	aca	aag	aga	tat	ttg	gac	ttt	gtt	caa	1440	
Glu	Lys	Tyr	Phe	Gly	Pro	Gln	Thr	Lys	Arg	Tyr	Leu	Asp	Phe	Val	Gln		
465				470				475				480					
tcg	gta	gaa	gga	gtt	acc	ggg	att	gga	atg	gtt	gta	cta	atg	acc	ata	1488	
Ser	Val	Glu	Gly	Val	Thr	Gly	Ile	Gly	Met	Val	Val	Leu	Met	Thr	Ile		
485				490				495									
gcc	ttt	aca	ttg	gct	aca	aca	tg	ttc	aga	cgt	aat	aag	ctc	aac	ctt	1536	
Ala	Phe	Thr	Leu	Ala	Thr	Thr	Trp	Phe	Arg	Arg	Asn	Lys	Leu	Asn	Leu		
500				505				510									
cct	gga	cca	ctg	aag	aaa	ata	aca	ggc	ttc	aat	gcc	ttc	tg	tac	tct	1584	
Pro	Gly	Pro	Leu	Lys	Lys	Ile	Thr	Gly	Phe	Asn	Ala	Phe	Trp	Tyr	Ser		
515				520				525									
cac	cac	tta	ttt	gtt	atc	gtc	tac	tcg	ctt	ctt	gtc	gtt	cat	gga	ttc	1632	
His	His	Leu	Phe	Val	Ile	Val	Tyr	Ser	Leu	Leu	Val	Val	His	Gly	Phe		
530				535				540									
tac	gta	tac	ctc	atc	atc	gag	cca	tg	tac	aag	aaa	acg	aca	tg	atg	1680	
Tyr	Val	Tyr	Leu	Ile	Ile	Glu	Pro	Trp	Tyr	Lys	Lys	Thr	Thr	Trp	Met		
545				550				555				560					
tat	ttg	atg	gta	ccg	gtg	gtt	ctt	tac	ttg	tgt	gaa	agg	ctg	att	cgt	1728	
Tyr	Leu	Met	Val	Pro	Val	Val	Leu	Tyr	Leu	Cys	Glu	Arg	Leu	Ile	Arg		
565				570				575									

gca ttc agg tca agc gtc gag gct gtt tca gtg cta aag gtt gct gtg	1776
Ala Phe Arg Ser Ser Val Glu Ala Val Ser Val Leu Lys Val Ala Val	
580 585 590	
tta cca ggg aat gtc ttg tcg ctt cac ttg tca aga cca agc aac ttc	1824
Leu Pro Gly Asn Val Leu Ser Leu His Leu Ser Arg Pro Ser Asn Phe	
595 600 605	
aga tac aag agt gga caa tac atg tat ctc aac tgt tct gca gtt tct	1872
Arg Tyr Lys Ser Gly Gln Tyr Met Tyr Leu Asn Cys Ser Ala Val Ser	
610 615 620	
aca tta gaa tgg cat cca ttc tca att acc tca gct cca gga gat gac	1920
Thr Leu Glu Trp His Pro Phe Ser Ile Thr Ser Ala Pro Gly Asp Asp	
625 630 635 640	
tac ctc agt gtc cac atc agg gtt tta gga gac tgg act aag caa tta	1968
Tyr Leu Ser Val His Ile Arg Val Leu Gly Asp Trp Thr Lys Gln Leu	
645 650 655	
aga tca tta ttc tct gag gtg tgc aag cca cgc cct cct gat gaa cac	2016
Arg Ser Leu Phe Ser Glu Val Cys Lys Pro Arg Pro Pro Asp Glu His	
660 665 670	
aga ctg aac aga gcc gac tcg aag cac tgg gat tac atc cct gac ttt	2064
Arg Leu Asn Arg Ala Asp Ser Lys His Trp Asp Tyr Ile Pro Asp Phe	
675 680 685	
cca aga atc cta att gat ggt cca tat gga gca cca gca caa gac tac	2112
Pro Arg Ile Leu Ile Asp Gly Pro Tyr Gly Ala Pro Ala Gln Asp Tyr	
690 695 700	
aag aag ttt gaa gtt gtt ctg cta gtg ggt cta gga atc ggt gcc act	2160
Lys Lys Phe Glu Val Val Leu Leu Val Gly Leu Gly Ile Gly Ala Thr	
705 710 715 720	
ccg atg atc agc ata gtg agt gac ata atc aat aac ttg aaa ggc gtg	2208
Pro Met Ile Ser Ile Val Ser Asp Ile Ile Asn Asn Leu Lys Gly Val	
725 730 735	
gaa gaa ggc agt aac cga aga cag tca ccg atc cat aat atg gtc aca	2256
Glu Glu Gly Ser Asn Arg Arg Gln Ser Pro Ile His Asn Met Val Thr	
740 745 750	
cct cct gtt tct cca tca aga aaa agt gag acg ttc aga acc aag aga	2304
Pro Pro Val Ser Pro Ser Arg Lys Ser Glu Thr Phe Arg Thr Lys Arg	
755 760 765	
gct tac ttc tac tgg gtc aca aga gag cag ggg tcg ttt gac tgg ttc	2352
Ala Tyr Phe Tyr Trp Val Thr Arg Glu Gln Gly Ser Phe Asp Trp Phe	
770 775 780	
aag aac gtg atg gac gaa gtg act gaa aca gac cgc aaa aac gta att	2400
Lys Asn Val Met Asp Glu Val Thr Glu Thr Asp Arg Lys Asn Val Ile	
785 790 795 800	
gag ctg cat aat tac tgc acc agc gtt tac gag gaa ggg gac gcg agg	2448
Glu Leu His Asn Tyr Cys Thr Ser Val Tyr Glu Glu Gly Asp Ala Arg	
805 810 815	
tct gca ctt atc acg atg ctc cag tct cta aac cat gct aag cat gga	2496
Ser Ala Leu Ile Thr Met Leu Gln Ser Leu Asn His Ala Lys His Gly	
820 825 830	
gtg gac gtt gtg tca gga aca cgt gtc atg tcc cat ttc gct agg cca	2544
Val Asp Val Val Ser Gly Thr Arg Val Met Ser His Phe Ala Arg Pro	
835 840 845	
aac tgg aga agc gtt ttc aaa agg atc gct gtg aat cat cct aag act	2592
Asn Trp Arg Ser Val Phe Lys Arg Ile Ala Val Asn His Pro Lys Thr	
850 855 860	
aga gtc gga gtg ttt tat tgt gga gca gct ggg tta gtg aaa gag tta	2640
Arg Val Gly Val Phe Tyr Cys Gly Ala Ala Gly Leu Val Lys Glu Leu	
865 870 875 880	
cga cac tta tca ctg gat ttc tct cat aag acc tcc acc aag ttc atc	2688
Arg His Leu Ser Leu Asp Phe Ser His Lys Thr Ser Thr Lys Phe Ile	
885 890 895	
ttc cat aaa gag aat ttc taa	2709

Phe His Lys Glu Asn Phe  
900

<210> 22

<211> 902

<212> PRT

<213> Arabidopsis thaliana

<400> 22

Met	Met	Asn	Arg	Ser	Glu	Met	Gln	Lys	Leu	Gly	Phe	Glu	His	Val	Arg
1				5					10					15	
Tyr	Tyr	Thr	Glu	Ser	Pro	Tyr	Asn	Arg	Gly	Glu	Ser	Ser	Ala	Asn	Val
			20					25					30		
Ala	Thr	Thr	Ser	Asn	Tyr	Tyr	Gly	Glu	Asp	Glu	Pro	Tyr	Val	Glu	Ile
		35					40					45			
Thr	Leu	Asp	Ile	His	Asp	Asp	Ser	Val	Ser	Val	Tyr	Gly	Leu	Lys	Ser
	50					55					60				
Pro	Asn	His	Arg	Gly	Ala	Gly	Ser	Asn	Tyr	Glu	Asp	Gln	Ser	Leu	Leu
	65				70					75					80
Arg	Gln	Gly	Arg	Ser	Gly	Arg	Ser	Asn	Ser	Val	Leu	Lys	Arg	Leu	Ala
				85					90					95	
Ser	Ser	Val	Ser	Thr	Gly	Ile	Thr	Arg	Val	Ala	Ser	Ser	Val	Ser	Ser
			100					105					110		
Ser	Ser	Ala	Arg	Lys	Pro	Pro	Arg	Pro	Gln	Leu	Ala	Lys	Leu	Arg	Arg
		115					120					125			
Ser	Lys	Ser	Arg	Ala	Glu	Leu	Ala	Leu	Lys	Gly	Leu	Lys	Phe	Ile	Thr
	130					135					140				
Lys	Thr	Asp	Gly	Val	Thr	Gly	Trp	Pro	Glu	Val	Glu	Lys	Arg	Phe	Tyr
	145				150					155					160
Val	Met	Thr	Met	Thr	Asn	Asn	Gly	Leu	Leu	His	Arg	Ser	Arg	Phe	Gly
				165					170					175	
Glu	Cys	Ile	Gly	Met	Lys	Ser	Thr	Glu	Phe	Ala	Leu	Ala	Leu	Phe	Asp
			180					185					190		
Ala	Leu	Ala	Arg	Arg	Glu	Asn	Val	Ser	Gly	Asp	Ser	Ile	Asn	Met	Asn
		195					200					205			
Glu	Leu	Lys	Glu	Phe	Trp	Lys	Gln	Ile	Thr	Asp	Gln	Asp	Phe	Asp	Ser
	210					215					220				
Arg	Leu	Arg	Thr	Phe	Phe	Ala	Met	Val	Asp	Lys	Asp	Ser	Asp	Gly	Arg
	225				230					235					240
Leu	Asn	Glu	Ala	Glu	Val	Arg	Glu	Ile	Ile	Thr	Leu	Ser	Ala	Ser	Ala
			245						250					255	
Asn	Glu	Leu	Asp	Asn	Ile	Arg	Arg	Gln	Ala	Asp	Glu	Tyr	Ala	Ala	Leu
		260						265					270		
Ile	Met	Glu	Glu	Leu	Asp	Pro	Tyr	His	Tyr	Gly	Tyr	Ile	Met	Ile	Glu
		275					280					285			
Asn	Leu	Glu	Ile	Leu	Leu	Leu	Gln	Ala	Pro	Met	Gln	Asp	Val	Arg	Asp
	290					295					300				
Gly	Glu	Ser	Lys	Lys	Leu	Ser	Lys	Met	Leu	Ser	Gln	Asn	Leu	Met	Val
	305				310					315					320
Pro	Gln	Ser	Arg	Asn	Leu	Gly	Ala	Arg	Phe	Cys	Arg	Gly	Met	Lys	Tyr
				325					330					335	
Phe	Leu	Phe	Asp	Asn	Trp	Lys	Arg	Val	Trp	Val	Met	Ala	Leu	Trp	Ile
			340					345					350		
Gly	Ala	Met	Ala	Gly	Leu	Phe	Thr	Trp	Lys	Phe	Met	Glu	Tyr	Arg	Lys
		355					360					365			
Arg	Ser	Ala	Tyr	Glu	Val	Met	Gly	Val	Cys	Val	Cys	Ile	Ala	Lys	Gly
	370					375					380				
Ala	Ala	Glu	Thr	Leu	Lys	Leu	Asn	Met	Ala	Met	Ile	Leu	Leu	Pro	Val
	385				390					395					400
Cys	Arg	Asn	Thr	Ile	Thr	Trp	Leu	Arg	Thr	Lys	Thr	Lys	Leu	Ser	Ala
				405					410						415

Ile	Val	Pro	Phe	Asp	Asp	Ser	Leu	Asn	Phe	His	Lys	Val	Ile	Ala	Ile
			420					425					430		
Gly	Ile	Ser	Val	Gly	Val	Gly	Ile	His	Ala	Thr	Ser	His	Leu	Ala	Cys
		435					440					445			
Asp	Phe	Pro	Arg	Leu	Ile	Ala	Ala	Asp	Glu	Asp	Gln	Tyr	Glu	Pro	Met
	450					455					460				
Glu	Lys	Tyr	Phe	Gly	Pro	Gln	Thr	Lys	Arg	Tyr	Leu	Asp	Phe	Val	Gln
465				470						475					480
Ser	Val	Glu	Gly	Val	Thr	Gly	Ile	Gly	Met	Val	Val	Leu	Met	Thr	Ile
			485					490							495
Ala	Phe	Thr	Leu	Ala	Thr	Thr	Trp	Phe	Arg	Arg	Asn	Lys	Leu	Asn	Leu
			500					505					510		
Pro	Gly	Pro	Leu	Lys	Lys	Ile	Thr	Gly	Phe	Asn	Ala	Phe	Trp	Tyr	Ser
		515					520					525			
His	His	Leu	Phe	Val	Ile	Val	Tyr	Ser	Leu	Leu	Val	Val	His	Gly	Phe
	530					535					540				
Tyr	Val	Tyr	Leu	Ile	Ile	Glu	Pro	Trp	Tyr	Lys	Lys	Thr	Thr	Trp	Met
545				550						555					560
Tyr	Leu	Met	Val	Pro	Val	Val	Leu	Tyr	Leu	Cys	Glu	Arg	Leu	Ile	Arg
			565						570					575	
Ala	Phe	Arg	Ser	Ser	Val	Glu	Ala	Val	Ser	Val	Leu	Lys	Val	Ala	Val
			580					585					590		
Leu	Pro	Gly	Asn	Val	Leu	Ser	Leu	His	Leu	Ser	Arg	Pro	Ser	Asn	Phe
		595				600						605			
Arg	Tyr	Lys	Ser	Gly	Gln	Tyr	Met	Tyr	Leu	Asn	Cys	Ser	Ala	Val	Ser
	610					615					620				
Thr	Leu	Glu	Trp	His	Pro	Phe	Ser	Ile	Thr	Ser	Ala	Pro	Gly	Asp	Asp
625				630						635					640
Tyr	Leu	Ser	Val	His	Ile	Arg	Val	Leu	Gly	Asp	Trp	Thr	Lys	Gln	Leu
			645						650					655	
Arg	Ser	Leu	Phe	Ser	Glu	Val	Cys	Lys	Pro	Arg	Pro	Pro	Asp	Glu	His
			660					665					670		
Arg	Leu	Asn	Arg	Ala	Asp	Ser	Lys	His	Trp	Asp	Tyr	Ile	Pro	Asp	Phe
		675				680						685			
Pro	Arg	Ile	Leu	Ile	Asp	Gly	Pro	Tyr	Gly	Ala	Pro	Ala	Gln	Asp	Tyr
	690					695					700				
Lys	Lys	Phe	Glu	Val	Val	Leu	Leu	Val	Gly	Leu	Gly	Ile	Gly	Ala	Thr
705				710						715					720
Pro	Met	Ile	Ser	Ile	Val	Ser	Asp	Ile	Ile	Asn	Asn	Leu	Lys	Gly	Val
			725						730					735	
Glu	Glu	Gly	Ser	Asn	Arg	Arg	Gln	Ser	Pro	Ile	His	Asn	Met	Val	Thr
			740					745					750		
Pro	Pro	Val	Ser	Pro	Ser	Arg	Lys	Ser	Glu	Thr	Phe	Arg	Thr	Lys	Arg
		755					760					765			
Ala	Tyr	Phe	Tyr	Trp</											

900

<210> 23  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Description of the artificial sequence:  
oligonucleotide primer

<400> 23  
garcaaggct cttttgattg

20

<210> 24  
<211> 21  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Description of the artificial sequence:  
oligonucleotide primer

<400> 24  
gaaatgctcc ttatggaatt c

21